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(54) Title: METHODS OF REDUCING FACTOR VIII CLEARANCE AND COMPOSITIONS THEREFOR

(54) Titre: PROCEDES DE REDUCTION DE LA CLAIRANCE DU FACTEUR VIII ET COMPOSITIONS CORRESPONDANTES

(57) Abstract

The present invention provides methods of increasing the half-life of factor VIII. More specifically, the invention provides methods of increasing the half-life of factor VIII by substituting amino acids in the A2 domain or in the C2 domain of factor VIII or in both domains. It further provides factor VIII mutants produced by these methods. The invention also provides a method of using receptor-associated protein (RAP) to increase the half-life of factor VIII. The invention also provides polynucleotides encoding the mutant factor VIII, polynucleotides encoding RAP, and methods of treating hemophilia using the polypeptides and polynucleotides of the invention.

(57) Abrégé

L'invention concerne des procédés permettant d'augmenter la demi-vie du facteur VIII. Plus spécifiquement, l'invention concerne des procédés qui permettent d'augmenter la demi-vie du facteur VIII en substituant des acides aminés dans le domaine A2 ou le domaine C2 du facteur VIII ou dans les deux domaines. En outre, l'invention concerne des mutants du facteur VIII élaborés par le biais des procédés considérés, et elle concerne un procédé relatif à l'utilisation d'une protéine associée au récepteur pour augmenter la demi-vie du facteur VIII. L'invention concerne enfin des polynucléotides codant le facteur VIII mutant, des polynucléotides codant la protéine associée au récepteur, et des procédés relatifs au traitement de l'hémophilie par le biais des polypeptides et des polynucléotides décrits.

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(54) Title: METHODS OF REDUCING FACTOR VIII CLEARANCE AND COMPOSITIONS THEREFOR

(57) Abstract: The present invention provides methods of increasing the half-life of factor VIII. More specifically, the invention provides methods of increasing the half-life of factor VIII by substituting amino acids in the A2 domain or in the C2 domain of factor VIII or in both domains. It further provides factor VIII mutants produced by these methods. The invention also provides a method of using receptor-associated protein (RAP) to increase the half-life of factor VIII. The invention also provides polynucleotides encoding the mutant factor VIII, polynucleotides encoding RAP, and methods of treating hemophilia using the polypeptides and polynucleotides of the invention.

Description

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**Methods of Reducing Factor VIII
Clearance and Compositions Therefor**10
*Statement as to Rights to Inventions Made Under
Federally-Sponsored Research and Development*5
Part of the work performed during development of this invention utilized
U.S. Government funds. The U.S. Government has certain rights in this
invention.

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*Background of the Invention*20
*Field of the Invention*10
This invention relates generally to a mutant factor VIII having increased
half-life, methods of production, pharmaceutically acceptable compositions and
uses thereof. This invention also relates to a method of using receptor associated
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protein to increase the half-life of factor VIII, methods of production,
pharmaceutically acceptable compositions and uses thereof.30
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*Related Art*35
Coagulation of blood occurs by either the "intrinsic pathway" or the
"extrinsic pathway," whereby certain blood proteins interact in a cascade of
proteolytic activations to ultimately convert soluble fibrinogen to insoluble fibrin.
These threads of fibrin are cross-linked to form the scaffolding of a clot; without
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fibrin formation, coagulation cannot occur.40
The intrinsic pathway consists of seven steps: (1) the proteolytic activation
of factor XII; (2) activated factor XII cleaves factor XI to activate it; (3) activated
factor XI cleaves factor IX, thereby activating it; (4) activated factor IX interacts
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with activated factor VIII to cleave and activate factor X; (5) activated factor X
binds to activated factor V on a membrane surface, which complex proteolytically
cleaves prothrombin to form thrombin; (6) thrombin proteolytically cleaves
fibrinogen to form fibrin; (7) fibrin monomers assemble into fibrils, which are
then cross-linked by factor XIII.

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The extrinsic pathway consists of the following steps: (1) upon rupture of a blood vessel, factor VII binds to tissue factor, a lipoprotein present in tissues outside the vascular system; (2) factor VII is activated to factor VIIa by proteolytic cleavage; and (3) the factor VIIa-tissue factor complex cleaves and activates factor X. Thereafter, the extrinsic pathway is identical to the intrinsic pathway, *i.e.* the two pathways share the last three steps described above.

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The plasma glycoprotein factor VIII circulates as an inactive precursor in blood, bound tightly and non-covalently to von Willebrand factor. Factor VIII (fVIII) is proteolytically activated by thrombin or factor Xa, which dissociates it from von Willebrand factor (vWF) and activates its procoagulant function in the cascade. In its active form, factor VIIIa (fVIIIa) functions as a cofactor for the factor X activation enzyme complex in the intrinsic pathway of blood coagulation, and it is decreased or nonfunctional in patients with hemophilia A.

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In hemophilia, blood coagulation is impaired by a deficiency in certain plasma blood coagulation factors. People with deficiencies in factor VIII or with antibodies against factor VIII suffer uncontrolled internal bleeding that may cause a range of serious symptoms unless they are treated with factor VIII. Symptoms range from inflammatory reactions in joints to early death. The classic definition of factor VIII, in fact, is that substance present in normal blood plasma that corrects the clotting defect in plasma derived from individuals with hemophilia A. A deficiency in vWF can also cause phenotypic hemophilia A because vWF is an essential component of functional factor VIII. In these cases, the half-life of factor VIII is decreased to such an extent that it can no longer perform its particular functions in blood-clotting.

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The fVIII protein consists of a homologous A and C domains and a unique B domain which are arranged in the order A1-A2-B-A3-C1-C2 (Vchar. G.A., *et al.*, *Nature* 312:337-340 (1984)). It is processed to a series of Me²⁺ linked heterodimers produced by cleavage at the B-A3 junction (Fay, P.J., *et al.*, *Biochem. Biophys. Acta* 871:268-278 (1986)), generating a light chain (LCh)

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consisting of an acidic region (AR) and A3, C1, and C2 domains and a heavy chain (HCh) which consists of the A1, A2, and B domains (Fig. 1).

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Activation of fVIII by thrombin leads to dissociation of activated fVIII (fVIIIa) from vWF and at least a 100-fold increase of the cofactor activity. The fVIIIa is a A1/A2/A3-C1-C2 heterotrimer (Fay, P.J., *et al.*, *J. Biol. Chem* 266:8957-8962 (1991)) in which domains A1 and A3 retain the metal ion linkage (Fig. 1) and the stable dimer A1/A3-C1-C2 is weakly associated with the A2 subunit through electrostatic forces (Fay, P.J., *et al.*, *J. Biol. Chem* 266:8957-8962 (1991)). Spontaneous dissociation of the A2 subunit from the heterotrimer results in non- proteolytic inactivation of fVIIIa.

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Infusion of fVIII/vWF complex or purified plasma or recombinant fVIII into patients with severe hemophilia A who do not have fVIII (Fijnvandraat, K., *et al.*, *Thromb. Haemostas.* 77:298-302 (1997); Morfini, M., *et al.*, *Thromb. Haemostas.* 68:433-435 (1992)) or in normal individuals (Over, J., *et al.*, *J. Clin. Invest.* 62:223-234 (1978)) results in a similar fVIII disappearance with a half-life of 12-14 hours. Although the complex between fVIII and vWF is crucial for normal half-life and level of factor VIII in the circulation, the mechanisms associated with turnover of fVIII/vWF complex are not well defined.

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The human factor VIII gene was isolated and expressed in mammalian

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cells (Toole, J. J., *et al.*, *Nature* 312:342-347 (1984); Gitschier, J., *et al.*, *Nature*

312:326-330 (1984); Wood, W. I., *et al.*, *Nature* 312:330-337 (1984); Vehar, G.

A., *et al.*, *Nature* 312:337-342 (1984); WO 87/04187; WO 88/08035; WO

88/03558; U.S. Pat. No. 4,757,006), and the amino acid sequence was deduced

from cDNA. Capon *et al.*, U.S. Pat. No. 4,965,199, disclose a recombinant DNA

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method for producing factor VIII in mammalian host cells and purification of

human factor VIII. Human factor VIII expression in CHO (Chinese hamster

ovary) cells and BHKC (baby hamster kidney cells) has been reported. Human

factor VIII has been modified to delete part or all of the B domain (U.S. Pat. No.

4,868,112), and replacement of the human factor VIII B domain with the human

factor V B domain has been attempted (U.S. Pat. No. 5,004,803). The cDNA

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sequence encoding human factor VIII and predicted amino acid sequence are
10 shown in SEQ ID NOS:1 and 2, respectively.

U.S. Patent No. 5,859,204, Lollar, J.S., describes mutants of human factor
VIII having reduced antigenicity and reduced immunoreactivity.

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Porcine factor VIII has been isolated and purified from plasma (Fass, D.
N., *et al.*, *Blood* 59:594 (1982)). Partial amino acid sequence of porcine factor
VIII corresponding to portions of the N-terminal light chain sequence having
homology to ceruloplasmin and coagulation factor V and largely incorrectly
located were described by Church, *et al.*, *Proc. Natl. Acad. Sci. USA* 81:6934
20 (1984). Toole, J. J., *et al.*, *Nature* 312:342-347 (1984) described the partial
sequencing of the N-terminal end of four amino acid fragments of porcine factor
VIII but did not characterize the fragments as to their positions in the factor VIII
25 molecule. The amino acid sequence of the B and part of the A2 domains of
porcine factor VIII were reported by Toole, J. J., *et al.*, *Proc. Natl. Acad. Sci. USA*
30 83:5939-5942 (1986). The cDNA sequence encoding the complete A2 domain
of porcine factor VIII and predicted amino acid sequence and hybrid
human/porcine factor VIII having substitutions of all domains, all subunits, and
specific amino acid sequences were disclosed in U.S. Pat. No. 5,364,771 by
35 Lollar and Runge, and in WO 93/20093. More recently, the nucleotide and
corresponding amino acid sequences of the A1 and A2 domains of porcine factor
VIII and a chimeric factor VIII with porcine A1 and/or A2 domains substituted
40 for the corresponding human domains were reported in WO 94/11503. U.S.
Patent No. 5,859,204, Lollar, J.S., discloses the porcine cDNA and deduced
amino acid sequences.

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Cellular endocytosis mediated by LRP was shown to be a mechanism of
removal of a number of structurally unrelated ligands including several proteins
45 related to coagulation or fibrilolysis. These ligands are: complexes of thrombin
with antithrombin III (ATIII), heparin cofactor II (HCII) (Kounnas, M.Z., *et al.*,
J. Biol. Chem. 271:6523-6529 (1996)), protease nexin I (Knauer, M.F., *et al.*, *J.*
50 *Biol. Chem.* 272:12261-12264 (1997)), complexes of urokinase-type and tissue-

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type plasminogen activators (u-PA and t-PA, respectively) with plasminogen activator inhibitor (PAI-1) (Nykaer, A., *et al.*, *J. Biol. Chem.* 267:14543-14546 (1992); Orth, K., *et al.*, *Proc. Natl. Acad. Sci.* 89:7422-7426 (1992)), thrombospondin (Mikhailenko, I., *et al.*, *J. Biol. Chem.* 272:6784-6791 (1997)), tissue factor pathway inhibitor (TFPI) (Warshawsky, I., *et al.*, *Proc. Natl. Acad. Sci.* 91:6664-6668 (1994)), and factor Xa (Narita, M., *et al.*, *Blood* 91:555-560 (1998); Ho, G., *et al.*, *J. Biol. Chem.* 271:9497-9502 (1996)).

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LRP, a large cell-surface glycoprotein identical to α_2 -macroglobulin receptor (Strickland, D.K., *et al.*, *J. Biol. Chem.* 265:17401-17404 (1990)), is a member of the low density lipoprotein (LDL) receptor family which also includes the LDL receptor, very low density lipoprotein (VLDL) receptor, vitellogenin receptor and glycoprotein 330 receptor. LRP receptor consists of the non-covalently linked 515 kDa α -chain (Hcrz, J., *et al.*, *EMBO J.* 7:4119-4127 (1988)) containing binding sites for LRP ligands, and the 85 kDa transmembrane β -chain.

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Within the α -chain, cluster of cysteine-rich class A repeats is responsible for ligand binding (Moestrup, S. K., *et al.*, *J. Biol. Chem.* 268:13691-13696 (1993)). In contrast to the acidic ligand binding region in LRP, ligands of LRP expose regions rich in positively charged amino acid residues (Moestrup, S.K., *Biochim. Biophys. Acta* 1197:197-213 (1994)). This type of binding and 31 class A repeats

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present in LRP may be responsible for its wide ligand diversity and ability to serve as a multi-ligand clearance receptor. LRP is expressed in many cell types and tissues including placenta, lung and brain (Moestrup, S.K., *et al.*, *Cell Tissue Res.* 269:375-382 (1992)) and is a major endocytic receptor in the liver (Strickland, D.K., *et al.*, *FASEB J.* 9:890-898 (1995)).

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A 39 kDa receptor-associated protein (RAP) binds to LRP with high affinity (K_d =4 nM (27)) and inhibits binding and LRP-mediated internalization and degradation of all ligands (Moestrup, S.K., *Biochim. Biophys. Acta* 1197:197-213 (1994); Williams, S.E., *et al.*, *J. Biol. Chem.* 267:9035-9040 (1992)), therefore serving as a useful tool for testing whether LRP is involved in endocytosis of a given ligand.

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Severe hemophiliacs, who number about 10,000 in the United States, can be treated with infusion of human factor VIII, vWF/factor VIII complex or vWF which will restore the blood's normal clotting ability if administered with sufficient frequency and concentration. However, supplies have been inadequate and problems in therapeutic use occur due to difficulty in isolation and purification, immunogenicity, and the necessity of removing the AIDS and hepatitis infectivity risk.

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Several preparations of human plasma-derived factor VIII of varying degrees of purity are available commercially for the treatment of hemophilia A. These include a partially-purified factor VIII derived from the pooled blood of many donors that is heat- and detergent-treated for viruses but contains a significant level of antigenic proteins; a monoclonal antibody-purified factor VIII that has lower levels of antigenic impurities and viral contamination; and recombinant human factor VIII, clinical trials for which are underway. Unfortunately, human factor VIII is unstable at physiologic concentrations and pH, is present in blood at an extremely low concentration (0.2 µg/ml plasma), and has low specific clotting activity.

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The problems associated with the commonly used, commercially available, plasma-derived factor VIII have stimulated significant interest in the development of a better factor VIII product. There is a need for a more potent factor VIII; a factor VIII that is stable at a selected pH and physiologic concentration; a factor VIII that has a longer half-life in circulating blood.

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Summary of the Invention

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The present invention relates to a method of increasing the half-life of factor VIII. More specifically, the present invention relates to a mutant of factor VIII having reduced clearance from plasma.

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In one embodiment, the mutant factor VIII has one or more amino acid substitutions in the A2 domain.

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10 In a preferred embodiment, the substituted amino acid(s) are important for receptor-dependent clearance of factor VIII, such that the resulting mutant factor VIII has a longer (increased) circulating half-life.

5 In another embodiment, the mutant factor VIII has one or more amino acid substitutions in the C2 domain.

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15 In a preferred embodiment, the substituted amino acid(s) are important for receptor-independent clearance of factor VIII, such that the resulting mutant factor VIII has a longer (increased) circulating half-life.

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10 In yet another preferred embodiment, amino acid(s) important for receptor-dependent clearance in the A2 domain and amino acid(s) important for receptor-independent clearance in the C2 domain are substituted, such that the resulting mutant factor VIII has an increased circulating half-life.

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15 The invention also relates to a method of using receptor associated protein (RAP) to increase the half-life of factor VIII. Further aspects of the invention include a method of producing factor VIII mutants having an increased half-life, pharmaceutically acceptable compositions thereof, and a method of treating factor 30 VIII deficiency using mutant factor VIII of the invention and/or RAP.

Brief Description of the Figures

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20 FIG. 1. Domain structure of fVIII and its fragments. The domain structure of mature fVIII protein is shown in line 1. The LCh acidic region is labeled as AR. Thrombin-cleaved LCh (A3-Cl-C2), heterotrimeric fVIIIa (A1/A2/3-Cl-C2) and heterodimer A1/A3-Cl-C2 are shown in lines 2, 3 and 4.

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45 FIGs. 2A and 2B. The amino acid sequence of mature, B-domainless fVIII (SEQ ID NO:5; composed from GenBank Accession No. X01179). The A2 sequence within fVIII is underlined and the sequence of the LRP binding site (residues 484-509) within A2 is indicated with asterisks. The amino acid residues shown as one-letter amino acid abbreviations.

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FIGS. 3A and 3B. The deduced amino acid sequence of full-length factor VIII (SEQ ID NO:2; from GenPep Accession No. CAA25619.1 and GenBank Accession No. X01179).

FIG. 4. The deduced amino acid sequence of RAP (SEQ ID NO:4; GenBank Accession No. M63959). The signal sequence (amino acids 1-34) is underlined and the LDL receptor binding region (amino acids 237-353) is indicated with asterisks.

FIGS. 5A and 5B. Binding of ^{125}I -fVIII to purified LRP by ligand competition assay. ^{125}I -fVIII (1 nM) was incubated for 1 h at 37°C in wells coated with LRP (●) or BSA (○) in the presence of increasing concentrations of unlabeled competitors, fVIII (●, ○) or vWF (Δ). *panel A*, and RAP (●, ○), *panel B*. In the experiment (Δ), ^{125}I -fVIII was preincubated with vWF for 30 min at 37°C, prior to its addition to the wells. Following incubation, the wells were washed and ^{125}I -fVIII binding was determined. Binding of ^{125}I -fVIII in the presence of unlabeled fVIII, vWF, or RAP is expressed as the percentage of ^{125}I -fVIII binding, when no competitor was added. Each point represents the mean value of triplicates and the error bars display the standard deviation. The curves show a best fit of the data to a model describing heterologous ligand displacement from a single class of binding sites using the program LIGAND.

FIG. 6. Effect of fragments of fVIII on its binding to LRP. ^{125}I -fVIII (1 nM) and increasing concentrations of unlabeled HCh (●), A2 (▲), LCh (○) or A1/A3-Cl-C2 (Δ) were incubated with LRP as described in Fig. 5. Each point represents the mean value and the standard deviation of the triplicates. The data were fitted as in Fig. 5 to a model describing heterologous ligand displacement from a single class of binding sites with K_i values of 120 and 132 nM for HCh and A2, respectively.

FIGS. 7A and 7B. Effect of monoclonal antibodies and synthetic peptides on ^{125}I -fVIII binding to purified LRP. *Panel A*, ^{125}I -fVIII (1 nM) and increasing concentrations of mAbs 413 (●) or T5 (○) were added to LRP coated wells as described in Fig. 5. In the control experiment (Δ), ^{125}I -fVIII and increasing

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concentrations of mAb 413 were added to BSA coated wells. *Panel B*, ^{125}I -fVIII and increasing concentrations of synthetic peptides consisting of the A2 domain residues 484-509 (●) or 432-456 (○) were added to LRP coated wells. In the control experiment (Δ), ^{125}I -fVIII and increasing concentrations of the peptide 484-509 were added to BSA coated wells. In the panels A and B, binding of ^{125}I -fVIII in the presence antibodies or peptides is expressed as the percentage of its binding, when no competitor was added. The mean and standard deviation of the triplicate measurements are presented.

FIGS. 8A and 8B. Internalization and degradation of ^{125}I -fVIII/vWF complex by LRP-expressing (MEF) and LRP-deficient (PEA 13) fibroblasts. Wells containing 2×10^4 of each MEF (○, ●) or PEA 13 cells (Δ, ▲) were incubated with 1 nM ^{125}I -fVIII/vWF in the absence (closed symbols) or presence (opened symbols) of RAP (1 μM). ^{125}I -fVIII/vWF complex was prepared by incubation of ^{125}I -fVIII with unlabeled vWF at a molar ratio 1:50 for 30 min at 37°C. At the indicated times, the amounts of internalized ^{125}I -fVIII (*panel A*) and degraded ^{125}I -fVIII (*panel B*) by the MEF and PEA 13 fibroblasts were determined as described under Experimental Procedures. In the experiment (▽), degradation of ^{125}I -fVIII (1 nM) by MEF cells in the presence of (0.1 mM) chloroquine is shown. Each data point represents the mean and standard deviation of duplicate determinations.

FIGS. 9A and 9B. Comparison of internalization of isolated ^{125}I -fVIII and components of fVIII/vWF complex. Wells containing 2×10^5 of each MEF and PEA 13 cells were incubated with 1 nM of isolated ^{125}I -fVIII or 1 nM of fVIII/vWF complex formed by mixing either ^{125}I -fVIII (1 nM) with unlabeled vWF (50 nM) or ^{125}I -vWF (50 nM) with unlabeled fVIII (1 nM). Following incubation for 6 hours with MEF cells in the absence of RAP (open bars) or in the presence of 1 μM RAP (solid bars) or after incubation with PEA 13 cells (hatched bars) the amounts of internalized (*panel A*) and degraded (*panel B*) isolated ^{125}I -fVIII, and ^{125}I -fVIII or ^{125}I -vWF from the fVIII/vWF complex were determined as described

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in Fig. 8. The data shown are an average of duplicate determinations \pm standard deviation.

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FIGS. 10A and 10B. The A2 domain of fVIII inhibits the internalization and degradation of ^{125}I -fVIII/vWF complex by MEF fibroblasts. One nM of ^{125}I -fVIII/vWF complex was prepared as in Fig. 8 and incubated with 2×10^5 of MEF cells in presence of 1 μM of A2 (○), 1 μM of A1/A3-Cl-C2 (Δ), or in the absence of any competitor (●). At the indicated times, the amounts of internalized (*panel A*) and degraded ^{125}I -fVIII (*panel B*) were determined as in Fig. 8. Each data point represents the mean and standard deviation of duplicate determinations.

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FIGS. 11A-D. Internalization and degradation of ^{125}I -A2 by MEF fibroblasts and by LRP-expressing smooth muscle cells (SMC) and alveolar epithelial cells (T2). In the *panels A and B*, 2×10^5 of MEF (○, ●) or PEA 13 cells (Δ, ▲) were incubated with 10 nM ^{125}I -A2 in the absence (closed symbols) or presence (opened symbols) of RAP (1 μM). At the indicated times, the amounts of internalized ^{125}I -A2 (*panel A*) and degraded ^{125}I -A2 (*panel B*) by the MEF and PEA 13 fibroblasts were determined as described in Fig. 8. In the experiment (▽), degradation of ^{125}I -A2 by MEF cells in the presence (0.1 mM) chloroquine is shown. Each data point represents the mean and standard deviation of duplicate determinations. In the *panels C and D*, ^{125}I -A2 (10 nM) was incubated for 4 h at 37°C in the wells containing 3×10^5 SMC (solid bars) or T2 (open bars) cells in the presence or absence of RAP (1 mM). The amount of ^{125}I -A2 internalized (*panel C*) and degraded (*panel D*) by the cells was determined as in Fig. 8. The data shown are an average of duplicate determinations \pm standard deviation.

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FIGS. 11A-D. Internalization and degradation of ^{125}I -A2 by MEF fibroblasts and by LRP-expressing smooth muscle cells (SMC) and alveolar epithelial cells (T2). In the *panels A and B*, 2×10^5 of MEF (○, ●) or PEA 13 cells (Δ, ▲) were incubated with 10 nM ^{125}I -A2 in the absence (closed symbols) or presence (opened symbols) of RAP (1 μM). At the indicated times, the amounts of internalized ^{125}I -A2 (*panel A*) and degraded ^{125}I -A2 (*panel B*) by the MEF and PEA 13 fibroblasts were determined as described in Fig. 8. In the experiment (▽), degradation of ^{125}I -A2 by MEF cells in the presence (0.1 mM) chloroquine is shown. Each data point represents the mean and standard deviation of duplicate determinations. In the *panels C and D*, ^{125}I -A2 (10 nM) was incubated for 4 h at 37°C in the wells containing 3×10^5 SMC (solid bars) or T2 (open bars) cells in the presence or absence of RAP (1 mM). The amount of ^{125}I -A2 internalized (*panel C*) and degraded (*panel D*) by the cells was determined as in Fig. 8. The data shown are an average of duplicate determinations \pm standard deviation.

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FIGS. 12A and 12B. The effect of RAP on clearance of ^{125}I -A2 (A) or ^{125}I -fVIII/vWF (B) from plasma of mice. BALB/c mice were injected into the tail vein by sample containing ^{125}I -A2 (36 nM), *panel A*, or ^{125}I -fVIII/vWF (20 nM), *panel B*, in the absence (●) or presence (○) of RAP (267 μM). At indicated time points, blood (50 μl) was collected into 10 μl of 100 mM EDTA and an aliquot (50 μl) was counted for radioactivity. The percentage of ligand remaining in circulation was calculated considering radioactivity of the aliquot taken at 1 min

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FIGS. 12A and 12B. The effect of RAP on clearance of ^{125}I -A2 (A) or ^{125}I -fVIII/vWF (B) from plasma of mice. BALB/c mice were injected into the tail vein by sample containing ^{125}I -A2 (36 nM), *panel A*, or ^{125}I -fVIII/vWF (20 nM), *panel B*, in the absence (●) or presence (○) of RAP (267 μM). At indicated time points, blood (50 μl) was collected into 10 μl of 100 mM EDTA and an aliquot (50 μl) was counted for radioactivity. The percentage of ligand remaining in circulation was calculated considering radioactivity of the aliquot taken at 1 min

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FIGS. 12A and 12B. The effect of RAP on clearance of ^{125}I -A2 (A) or ^{125}I -fVIII/vWF (B) from plasma of mice. BALB/c mice were injected into the tail vein by sample containing ^{125}I -A2 (36 nM), *panel A*, or ^{125}I -fVIII/vWF (20 nM), *panel B*, in the absence (●) or presence (○) of RAP (267 μM). At indicated time points, blood (50 μl) was collected into 10 μl of 100 mM EDTA and an aliquot (50 μl) was counted for radioactivity. The percentage of ligand remaining in circulation was calculated considering radioactivity of the aliquot taken at 1 min

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FIGS. 12A and 12B. The effect of RAP on clearance of ^{125}I -A2 (A) or ^{125}I -fVIII/vWF (B) from plasma of mice. BALB/c mice were injected into the tail vein by sample containing ^{125}I -A2 (36 nM), *panel A*, or ^{125}I -fVIII/vWF (20 nM), *panel B*, in the absence (●) or presence (○) of RAP (267 μM). At indicated time points, blood (50 μl) was collected into 10 μl of 100 mM EDTA and an aliquot (50 μl) was counted for radioactivity. The percentage of ligand remaining in circulation was calculated considering radioactivity of the aliquot taken at 1 min

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after injection as 100%. The clearance of each preparation was examined in two mice, and the data plotted represent the average value \pm standard deviation.

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Detailed Description of the Preferred Embodiments

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5 "Factor VIII" (or "coagulation factor VIII"), as used herein, refers to a plasma glycoprotein that is a member of the intrinsic coagulation pathway and is essential to blood coagulation. A congenital X-linked deficiency of biologically active factor VIII results in Hemophilia A, a potentially life-threatening disorder.

20 Unless otherwise specified or indicated, as used herein, "factor VIII" denotes any functional human factor VIII protein molecule in its normal role in coagulation, including any fragment, analog derivative or modified factor VIII. The human factor VIII cDNA nucleotide and full-length predicted amino acid sequences are shown in SEQ ID NOs: 1 and 2, respectively. Human factor VIII peptides of the invention include full-length factor VIII, full-length factor VIII minus Met at the N-terminus, mature factor VIII (minus the signal sequence), mature factor VIII with an additional Met at the N-terminus, and/or factor VIII with or without a B domain. Factor VIII of the invention may also include porcine factor VIII. The cDNA and predicted amino acid sequences of the porcine factor VIII are disclosed in U.S. Patent No.,859,204.

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20 "Subunits" of factor VIII, as used herein, are the heavy and light chains of the protein. The heavy chain of factor VIII contains three domains, A1, A2, and B. The light chain of factor VIII also contains three domains, A3, C1, and C2. Factor VIII is synthesized as an approximately 300 kDa single chain protein with internal sequence homology that defines the "domain" sequence NH₂-A1-A2-B-A3-C1-C2-COOH.

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40 25 In a factor VIII molecule, a "domain", as used herein, is a continuous sequence of amino acids that is defined by internal amino acid sequence identity and sites of proteolytic cleavage by thrombin. Unless otherwise specified, factor VIII domains include the following amino acid residues: A1, residues

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Ala1-Arg372; A2, residues Ser373-Arg740; B, residues Ser741-Arg1648; A3, residues Ser1690-Ile2032; C1, residues Arg2033-Asn2172; C2, residues Ser2173-Tyr2332. The A3-C1-C2 sequence includes residues Ser1690-Tyr2332. The remaining sequence, residues Glu1649-Arg1689, is usually referred to as the factor VIII light chain activation peptide.

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A "B-domainless" factor VIII or "B (-)" factor VIII, or fragment of thereof, as used herein, refers to any one of the factor VIII mutants described herein that lacks the B domain. The amino acid sequence of mature, B (-) factor VIII as constructed from GenBank Accession No. X01179 is shown in Figure 2 (SEQ ID NO:5). B (-) factor VIII of the invention includes B (-) factor VIII with or without a signal sequence and with or without a Met at the N-terminus.

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As used herein, a "mutant factor VIII or fragment thereof" or "factor VIII mutant or fragment thereof" is an active factor VIII molecule or fragment thereof comprising at least one amino acid substitution.

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"RAP," as used herein, refers to the receptor-associated protein, also called the α_2 macroglobulin receptor-associated protein. RAP reduces receptor-dependent clearance of factor VIII. The human RAP deduced amino acid sequence is shown in Figure 4 (SEQ ID NO:4; GenBank Accession No. P30533). The RAP cDNA sequence is shown in SEQ ID NO:3 and GenBank Accession No. M63959. Mutant RAP proteins of the invention may have an amino acid substitution at one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, twenty or more positions of RAP. An amino acid substitution at "position" 327, for example, of RAP, refers to an amino acid substitution at amino acid 327 of the RAP amino acid sequence in GenBank Accession No. P30533.

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By "amino acid substitution" is meant a substitution of one amino acid for one of the remaining 19 naturally occurring amino acids. By an amino acid substitution at any one of positions "484 to 509," for example, is meant an amino acid substitution any position in the range, including at positions 484 and 509. The mutant factor VIII or RAP proteins of the invention may have an amino acid

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substitution at one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, twenty or more positions.

An amino acid substitution at "position" 499, for example, of factor VIII, refers to an amino acid substitution at position 499 according to the numbering system of Wood *et al.*, *Nature* 312:330-337 (1984).

"Half-life," as used herein, refers to the half-life of factor VIII in circulation, as determined in animals such as mice, for example, using the method of Examples 1 and 2. Factor VIII has a half-life of 12-14 hours. As provided herein, methods to increase the half-life of factor VIII would lead to a factor VIII half-life of longer than 12-14 hours.

"Receptor-dependant clearance," as used herein, refers to the receptor-mediated removal of factor VIII from circulation. As described in the examples, receptor-dependant clearance is exhibited by MEF cells, and is inhibited by RAP. Receptor-dependent clearance includes, but is not limited, to LRP-mediated clearance of factor VIII clearance. Additional receptors may be involved in receptor-dependent clearance.

"Receptor-independent clearance," as used herein, refers to the removal of factor VIII from circulation by means different from receptor-dependant clearance. RAP does not inhibit receptor-independent clearance.

"Factor VIII deficiency," as used herein, includes deficiency in clotting activity caused by production of defective factor VIII, by inadequate or no production of factor VIII, or by partial or total inhibition of factor VIII by inhibitors. Hemophilia A is a type of factor VIII deficiency resulting from a defect in an X-linked gene and the absence or deficiency of the factor VIII protein it encodes. A deficiency in vWF can also cause phenotypic hemophilia A because vWF is an essential component of functional factor VIII. In these cases, the half-life of factor VIII is decreased to such an extent that it can no longer perform its particular functions in blood-clotting.

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"Plasma," as used herein, refers to the fluid, non-cellular portion of the blood of humans or animals as found prior to coagulation. It is distinguished from serum, which is obtained after coagulation.

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5 "Pharmaceutically acceptable carrier," as used herein, refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type.

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"Patient," as used herein, refers to human or animal individuals receiving medical care and/or treatment.

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10 "Congenital deficiency," as used herein, refers to the condition of an individual that lacks, as a result of heredity, a compound found in normal individuals. Congenital deficiencies are permanent absent transplantation or genetic intervention, which at this time are not guaranteed cures.

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15 "Acquired deficiency," as used herein, refers to the condition of an individual that lacks, as a result of a non-congenital influence, a compound found in normal individuals. Acquired deficiencies are frequently the transient result of other conditions or their treatment, but are nonetheless debilitating and life threatening.

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20 A "fusion protein," as used herein, is the product of a gene in which the coding sequence for one protein is extensively altered, for example, by fusing part of it to the coding sequence for a second protein from a different gene to produce a gene that encodes the fusion protein. As used herein, a fusion protein is a subset of the factor VIII protein or RAP protein described in this application.

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25 A "corresponding" nucleic acid or amino acid or corresponding sequence of either, as used herein, is one present at a site in a factor VIII or mutant factor VIII molecule or fragment thereof that has the same structure and/or function as a site in the factor VIII molecule of another species, although the nucleic acid or amino acid number may not be identical.

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"Procoagulant activity," as used herein, refers to factor VIII coagulation activity exhibited in a human factor VIII assay.

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"Specific activity," as used herein, refers to the activity that will correct the coagulation defect of human factor VIII deficient plasma. Specific activity is measured in units of clotting activity per milligram total factor VIII protein in a standard assay in which the clotting time of human factor VIII deficient plasma is compared to that of normal human plasma. One unit of factor VIII activity is the activity present in one milliliter of normal human plasma. In the assay, the shorter the time for clot formation, the greater the activity of the factor VIII being assayed. Mutant factor VIII has coagulation activity in a human factor VIII assay. This activity may be less than, equal to, or greater than that of either plasma-derived or recombinant human factor VIII.

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the activity present in one milliliter of normal human plasma. In the assay, the shorter the time for clot formation, the greater the activity of the factor VIII being assayed. Mutant factor VIII has coagulation activity in a human factor VIII assay.

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This activity may be less than, equal to, or greater than that of either plasma-derived or recombinant human factor VIII.

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"Polypeptides," "molecules" and "proteins," as used herein, includes all polypeptides as described below. The basic structure of polypeptides is well known and has been described in innumerable textbooks and other publications in the art. In this context, the term is used herein to refer to any peptide or protein comprising two or more amino acids joined to each other in a linear chain by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types.

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comprising two or more amino acids joined to each other in a linear chain by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types.

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It will be appreciated that polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids, and that many amino acids, including the terminal amino acids, may be modified in a given polypeptide, either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques which are well known to the art. Even the common modifications that occur naturally in polypeptides are too numerous to list exhaustively here, but they are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. Among the known modifications which may be present in polypeptides of the present invention are, to name an illustrative few, acetylation, acylation,

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techniques which are well known to the art. Even the common modifications that occur naturally in polypeptides are too numerous to list exhaustively here, but they are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. Among the known modifications which may be present in polypeptides of the present invention are, to name an illustrative few, acetylation, acylation,

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of the present invention are, to name an illustrative few, acetylation, acylation,

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ADP-ribosylation, amidation, PEGylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formulation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

Such modifications are well known to those of skill and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as, for instance *Proteins - Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W.H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as, for example, those provided by Wold, F., Posttranslational Protein Modifications: Perspectives and Prospects, pp. 1-12 in *Posttranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter *et al.*, Analysis for protein modifications and nonprotein cofactors, *Meth. Enzymol.* 182: 626-646 (1990) and Rattan *et al.*, *Protein Synthesis: Post translational Modifications and Aging*, *Ann. N.Y. Acad. Sci.* 663: 48-62 (1992).

In general, as used herein, the term polypeptide encompasses all such modifications, particularly those that are present in polypeptides synthesized by expressing a polynucleotide in a host cell.

The invention also relates to fragments, "derivatives" and analogs of these polypeptides. The terms "fragment," "derivative" and "analog" when referring to the polypeptides of FIGS. 2, 3 or 4, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. A mutant, fragment

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derivative or analog of factor VIII refers to a polypeptide that retains factor VIII procoagulant activity. A mutant, fragment derivative or analog of RAP refers to a polypeptide that retains the ability to reduce receptor-dependent clearance of factor VIII. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide. Fragments, derivatives and analogs are described in detail herein.

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A fragment, derivative or analog of the polypeptide of the invention may be (i) one in which one or more of the amino acid residues includes a substituent group, or (ii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iii) one in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

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The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide. In certain preferred embodiments it is a recombinant polypeptide.

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Further particularly preferred in this regard are mutants, analogs and fragments; and mutants and analogs of the fragments, having the defined activity and/or having the amino acid sequence of the polypeptides of FIGS. 2, 3 or 4.

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The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

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"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, polynucleotides as used herein refers to, among others, single-and double-stranded DNA, DNA that is a mixture of single-and double-stranded regions, single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising

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DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, polynucleotide as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide.

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As used herein, the term polynucleotide includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein.

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It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*.

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Polynucleotides of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

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Polynucleotides of the present invention may include, but are not limited to the coding sequence for the mature polypeptide, by itself, the coding sequence for the mature polypeptide and additional coding sequences, such as those encoding a leader or secretory sequence, such as a pre-, or pro- or prepro- protein sequence; the coding sequence of the mature polypeptide, with or without the

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aforementioned additional coding sequences, together with additional, non-coding sequences, including for example, but not limited to introns and non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences that play a role in transcription, mRNA processing--including splicing and polyadenylation signals, for example--ribosome binding and stability of mRNA; additional coding sequence which codes for additional amino acids, such as those which provide additional functionalities. Thus, for instance, the polypeptide may be fused to a marker sequence, such as a peptide, which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexahistidine peptide, such as the tag provided in a pQE vector (Qiagen, Inc.), among others, many of which are commercially available. As described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. The HA tag corresponds to an epitope derived of influenza hemagglutinin protein, which has been described by Wilson *et al.*, *Cell* 37: 767 (1984), for instance.

An "effective amount" of an agent, as used herein, is an amount of such agent that is sufficient to bring about a desired result, especially upon administration of such agent to an animal or human.

The term "administration" is meant to include introduction of polypeptides or polynucleotides of the invention into an animal or human by any appropriate means known to the medical art, including, but not limited to, injection, oral, enteral, transdermal and parenteral (e.g., intravenous) administration.

The term "pharmaceutically acceptable salt" is intended to include salts of the mutant factor VIII or RAP of the invention. Such salts can be formed from pharmaceutically acceptable acids or bases, such as, for example, acids such as sulfuric, hydrochloric, nitric, phosphoric, etc., or bases such as alkali or alkaline earth metal hydroxides, ammonium hydroxides, alkyl ammonium hydroxides, etc.

The term "pharmaceutically acceptable composition" is intended to include solvents, carriers, diluents, and the like, which are utilized as additives or vehicles to preparations of the mutant factor VIII or RAP of the invention so as

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to provide a carrier or adjuvant for the administration of such compounds to patients (human or animal) in need of the same. Such additives can perform certain functions, such as, for example, provide the proper ionic conditions for administration, stabilize the mutant factor VIII or RAP against inactivation or degradation, and/or increase the half-life of the mutant factor VIII or RAP. A pharmaceutically acceptable composition is medically compatible with the host to which it is being administered.

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10 The term "treatment" or "treating" is intended to include the administration of the pharmaceutically acceptable compositions of the invention comprising effective amounts of mutant factor VIII or RAP (polypeptides or polynucleotides) of the invention to a patient for purposes which may include prophylaxis, amelioration, prevention or cure of a medical disorder.

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15 A material is said to be "substantially free of natural contaminants" if it has been substantially purified from materials with which it is normally and naturally found before such purification and those contaminants normally and naturally found with the substance *in vivo* or *in vitro* are substantially absent from the final preparation of the material. When administered to a subject in need of treatment, the mutant factor VIII or RAP of the invention is substantially free of natural contaminants which associate with the mutant factor VIII or RAP either *in vivo* (in the host from which the mutant factor VIII or RAP was isolated), or *in vitro* (as a result of a chemical synthesis). By "substantially absent" is meant that such contaminants are either completely absent or are present at such low concentrations that their presence (1) does not interfere with the desired therapeutic effect of the active agent in the therapeutically acceptable composition when such composition is administered to a patient in need of same and (2) does not harm the patient as the result of the administration of such composition.

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Since current information indicates that the B domain has no known effect on factor VIII function, in some embodiments the B domain is deleted ("B domain (-)" or "B domainless") in the mutant factor VIII molecule or fragments

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thereof ("B(-) factor VIII" or "B domainless factor VIII") prepared by any of the methods described herein.

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Generation of mutant(s) with a prolonged lifetime may be a promising approach to increase the efficacy and reduce the cost of fVIII infusion therapy.

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The invention provides methods of increasing the half-life of factor VIII by mutating factor VIII, and further provides methods of increasing the half-life of factor VIII using receptor-associated protein (RAP).

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Factor VIII Mutants: A2 Domain

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A recombinant mutant factor VIII having reduced receptor-dependent clearance and/or reduced receptor-independent clearance, and/or having superior coagulant activity compared to human factor VIII, may be less expensive to make than plasma-derived factor VIII and may decrease the amount of factor VIII required for effective treatment of factor VIII deficiency.

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The present invention provides active recombinant mutant factor VIII molecules or fragments thereof comprising at least one amino acid substitution in the A2 domain, polynucleotides encoding these, methods of producing and isolating them, and methods for characterizing their coagulant and plasma clearance properties.

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The A2 domain is necessary for the procoagulant activity of the factor VIII molecule. Studies show that porcine factor VIII has six-fold greater procoagulant activity than human factor VIII (Lollar, P., and E. T. Parker 266 J. Biol. Chem. 12481-12486 (1991)), and that the difference in coagulant activity between human and porcine factor VIII appears to be based on a difference in amino acid sequence between one or more residues in the human and porcine A2 domains (Lollar, P., *et al.*, 267 J. Biol. Chem. 23652-23657 (1992)).

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In one embodiment, the invention provides a method of increasing the half-life of factor VIII by substituting amino acids in the factor VIII A2 domain. In another embodiment, the invention provides mutant factor VIII and fragments thereof, and the polynucleotides encoding same, which have an increased

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circulating half-life than human factor VIII. The increased circulating half-life is due to a reduction in receptor-dependent clearance of factor VIII. As shown in the examples, amino acids in the factor VIII A2 domain interact with at least one receptor that mediates A2 clearance and factor VIII clearance from plasma.

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5 Thus, factor VIII mutants of the invention include mutants with one or more substitutions within the A2 domain. In a preferred embodiment, the factor VIII mutants have an amino acid substitution at one or more positions from 484 to 509. This region includes the following sequence: NH₂- Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe -COOH.

10 In another preferred embodiment, the factor VIII mutants have an amino acid substitution at one or more of positions 484, 489, 490, 493, 496 or 499.

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15 The amino acid at a particular position is substituted with any of the 19 other naturally occurring amino acids. A2 amino acid substitutions of the invention are those that inhibit the interaction of factor VIII with its clearance receptor(s). Thus, nonconservative A2 amino acid substitutions are preferred over conservative substitutions. Conservative amino acid substitutions include, for example, the substitution of an acidic amino acid with another acidic amino acid, a basic amino acid with another basic amino acid, a hydrophobic amino acid with another hydrophobic amino acid, a polar amino acid with another polar amino acid, or an aromatic amino acid with another aromatic amino acid. Conservative amino acid substitutions are well known in the art.

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20 Thus, an example of a conservative substitution is the substitution of Lys with Arg, while an example of a preferred nonconservative substitution is the substitution of Lys with Asp, Glu, Tyr, Asn, Gln, Thr, Ser, Cys, Trp, Phe, Pro, Met, Val, Leu, Ile, Trp, Gly or Ala.

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25 Preferred A2 amino acid substitutions of the invention are the substitution of Lys or Arg with Leu, Ile or Val. Additional preferred A2 amino acid substitutions of the invention are the substitutions of Lys or Arg with Asp or Glu.

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Further preferred amino acid substitutions of the invention are the substitution of Lys or Arg with Ala. Ser, Thr, Met or Gly.

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In another embodiment, amino acids at positions outside 484-509 are substituted, such as at positions 480, 481, 482, 483, 510, 511, 512 or 513.

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Preferred substitutions at these positions are those that reduce receptor-dependent clearance of factor VIII, such as introducing bulky or negatively charged amino acids.

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Specifically provided as an exemplary and a preferred embodiment is active recombinant human factor VIII having substituted amino acids in the A2 domain, the polynucleotide encoding it, and the methods of producing, isolating, and characterizing its activity. The methods by which this mutant is prepared can also be used to prepare active recombinant factor VIII or fragments thereof having substituted amino acids in domains other than A2. One skilled in the art will recognize that these methods also demonstrate how other recombinant mutant factor VIII molecules or fragments thereof can be prepared in which amino acids are substituted. Additionally, recombinant methods are described in *Current Protocols in Molecular Biology*, F. M. Ausubel *et al.*, eds. (1991); and Sambrook, J., *et al.*, *Molecular Cloning. A Laboratory Manual*.

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Mutant factor VIII is prepared starting with human cDNA (Biogen, Inc.) encoding the factor VIII sequence. In a preferred embodiment, the factor VIII encoded by this cDNA includes domains A1-A2-A3-C1-C2, lacking the entire B domain, and corresponds to amino acid residues 1-740 and 1649-2332 of single chain human factor VIII (see SEQ ID NO:2), according to the numbering system of Wood *et al.*, 312 *Nature* 330-337 (1984).

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The mutant factor VIII cDNA are cloned into expression vectors for ultimate expression of active factor VIII protein molecules in cultured cells by established techniques, as described by Selden, R.F., "Introduction of DNA into mammalian cells," in *Current Protocols in Molecular Biology*, F.M. Ausubel *et al.*, eds (1991).

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In a preferred embodiment, a cDNA encoding mutant factor VIII is inserted in a mammalian expression vector, such as ReNeo, to form a mutant factor VIII construct. Preliminary characterization of the mutant factor VIII is accomplished by insertion of the mutant cDNA into the mammalian expression vector and transient expression of the mutant protein in COS-7 cells. A determination of whether active protein is expressed can then be made. The expression vector construct is used further to stably transfet cells in culture, such as baby hamster kidney cells, using methods that are routine in the art, such as liposome-mediated transfection (Lipofectin™, Life Technologies, Inc.). Expression of recombinant mutant factor VIII protein can be confirmed, for example, by sequencing, Northern and Western blotting, or polymerase chain reaction (PCR). Mutant factor VIII protein in the culture media in which the transfected cells stably expressing the protein are maintained can be precipitated, pelleted, washed, and resuspended in an appropriate buffer, and the recombinant mutant factor VIII protein purified by standard techniques, including immunaffinity chromatography using, for example, monoclonal anti-A2-Sepharose™.

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In a further embodiment, the mutant factor VIII comprising amino acid substitutions is expressed as a fusion protein from a recombinant molecule in which sequence encoding a protein or peptide that enhances, for example, stability, secretion, detection, isolation, or the like is inserted in place adjacent to the factor VIII encoding sequence. Established protocols for use of homologous or heterologous species expression control sequences including, for example, promoters, operators, and regulators, in the preparation of fusion proteins are known and routinely used in the art. (See *Current Protocols in Molecular Biology*, Ausubel, F.M., et al., eds, Wiley Interscience, N.Y.)

Other vectors, including both plasmid and eukaryotic viral vectors, may be used to express a recombinant gene construct in eukaryotic cells depending on the preference and judgment of the skilled practitioner (see, for example, Sambrook et al., Chapter 16). Other vectors and expression systems, including

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10 bacterial, yeast, and insect cell systems, can be used but are not preferred due to
differences in, or lack of, glycosylation.

10 The purified mutant factor VIII or fragment thereof can be assayed for
amount and for coagulation activity by standard assays including, for example,
5 the plasma-free factor VIII assay, the one-stage clotting assay, and the
enzymic-linked immunosorbent assay using purified recombinant human factor
15 VIII as a standard.

20 Recombinant mutant factor VIII protein can be expressed in a variety of
cells commonly used for culture and recombinant mammalian protein expression.

20 10 A preferred cell line, available from the American Type Culture Collection,
Rockville, Md., is baby hamster kidney cells, which are cultured using routine
procedure and media.

25 Any mutant factor VIII construct having an amino acid substitution at one
or more positions in the A 2 domain as described can be assayed by standard
15 procedures for coagulant activity and may be assayed for receptor-dependent
30 clearance as described herein to identify mutant factor VIII molecules with
enhanced coagulant activity and/or reduced receptor-mediated clearance. Mutant
molecules may also be identified that have reduced coagulant activity compared
35 to human or porcine factor VIII but also have reduced receptor-mediated
clearance. One skilled in the art will recognize that mutant factor VIII molecules
40 or fragments thereof having less, equal, or greater coagulant activity, compared
45 to human or porcine factor VIII, is useful for treating patients who have a factor
VIII deficiency. The methods described herein to prepare active recombinant
mutant factor VIII with amino acid substitution(s) in the A2 domain can be used
50 to prepare active recombinant mutant factor VIII protein with amino acid
substitution(s) in the C2 domain or fragments thereof.

55 These molecules can be expressed in COS-7 cells and baby hamster
kidney cells as described above. They can be purified to homogeneity using
methods known in the art, such as heparin-Sepharose™ and immunoaffinity
chromatography. Protein concentration can be estimated by absorption of

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ultraviolet light at A_{280} , and the specific activity of the constructs can be determined by dividing coagulant activity (measured in units per ml by single stage clotting assay) by A_{280} . Human factor VIII has a specific activity of approximately 3000-4000 U/ A_{280} , whereas porcine factor VIII has a specific activity of approximately 20,000 U/ A_{280} . In a preferred embodiment, the coagulant mutant factor VIII has a specific activity of 3000 U/ A_{280} . In a preferred embodiment, the coagulant mutant factor VIII has a specific activity of 3000 U/ A_{280} . The a specific activity of mutant factor VIII may be anywhere in the range of 1000-20,000 U/ A_{280} .

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10 As described herein, site-directed mutagenesis techniques are used to identify mutant protein with coagulant activity that can be enhanced, equal to, or reduced, compared to human factor VIII, but preferably is enhanced. Oligonucleotide-directed mutagenesis can be used as described in Kunkel, T.A., et al., *Meth. Enzymol.* 204:125-139 (1991).

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15 The mutant factor VIII proteins of the invention may have an amino acid substitution at one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, twenty or more positions of factor VIII. The mutant factor VIII molecules of the invention may have amino acid substitutions in more than one domain, such as having an amino acid substitution both in the A2 domain and in the C2 domain.

The present invention contemplates that mutant factor VIII cDNA and protein can be characterized by methods that are established and routine, such as DNA sequencing, coagulant activity assays, mass by ELISA and by UV absorbency at 280 nm of purified mutant factor VIII, specific coagulant activity (U/mg), SDS-PAGE of purified mutant factor VIII, and the like. Other known methods of testing for clinical effectiveness may be required, such as amino acid, carbohydrate, sulfate, or metal ion analysis.

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Factor VIII Mutants: C2 Domain

10 The same methods employed for preparing mutant human factor VIII having A2 domain amino acid substitution(s) can be used to prepare other recombinant mutant factor VIII protein and fragments thereof and the 5 polynucleotides encoding these, such as mutant factor VIII having amino acid substitutions in the C2 domain.

15 Mutant human factor VIII molecules with amino acid substitution(s) in the C2 domain, which have reduced or no receptor-independent clearance can be identified. More specifically, the procedures can be the same or similar to those 20 described herein for amino acid substitution in the A2 domain (by alanine scanning mutagenesis, site-directed mutagenesis, etc.,) substituting amino acids in the C2 domain of B (-) factor VIII; insertion into an expression vector, such as 25 pBluescript; expression in cultured cells; and routine assay for coagulant activity and receptor-independent clearance.

30 15 In one embodiment, the invention provides mutant factor VIII and fragments thereof, and the polynucleotides encoding same, which have an increased circulating half-life than human factor VIII. The increased circulating half-life of mutant factor VIII is due to a reduction in receptor-independent 35 clearance of factor VIII.

40 20 The C2 domain consists of amino acid residues 2173-2332. Within this 154 amino acid region, positions 2303-2332 are involved in both phospholipid binding and vWF binding. A synthetic peptide of factor VIII amino acids 2310-45 2320 (in which residues 2310 and 2320 are covalently linked) competes with factor VIII for phospholipid binding. A comparison of factor V, which does not bind vWF, and factor VIII reveals 5 amino acids within positions 2311-2319 that are unique to factor VIII. Although not being bound by any theory, these unique 50 positions (Gln2311, Ser 2312, Val 2314, His2315 and Gln2316) are important for receptor-independent clearance, but are not critical for vWF binding.

30 Thus, one embodiment of the present invention is a mutant factor VIII having an amino acid substitution at one or more of positions 2173-2332 in the

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10 C2 domain. In another preferred embodiment, the mutant factor VIII has an amino acid substitution at one or more positions 2311-2319 in the C2 domain.

15 The amino acid at a particular position is substituted with any of the 19 other naturally occurring amino acids. C2 amino acid substitutions of the invention are those that inhibit the interaction of factor VIII with phospholipid.

20 Thus, nonconservative C2 amino acid substitutions are preferred over conservative substitutions. Conservative amino acid substitutions include, for example, the substitution of an acidic amino acid with another acidic amino acid, a basic amino acid with another basic amino acid, a hydrophobic amino acid with another hydrophobic amino acid, a polar amino acid with another polar amino acid, or an aromatic amino acid with another aromatic amino acid. Conservative amino acid substitutions are well known in the art.

25 Thus, an example of a conservative substitution is the substitution of Leu with Ile or Val, while an example of a preferred nonconservative substitution is the substitution of Leu with Asp, Glu, Arg, Lys, His, Tyr, Asn, Gln, Thr, Ser, Cys, Trp, Phe, Pro, Met, Trp, Gly or Ala. One preferred substitution is Ala.

30 Additional embodiments of the present invention include a method of treating hemophilia by administering a C2 domain mutant of factor VIII, pharmaceutically acceptable compositions comprising a C2 domain mutant of factor VIII either alone or in combination with RAP, and polynucleotides encoding a C2 domain mutant of factor VIII.

35 Furthermore, the amino acid substitution(s) in the C2 domain can be combined with amino acid substitution(s) in the A2 domain, to produce a mutant factor VIII with increased half-life.

40

25 ***Receptor Associated Protein***

45 A preferred embodiment of the present invention is directed to a method of increasing the half-life of factor VIII by administering RAP. Preferably, the RAP binds LRP, more preferably, the RAP has an increased affinity for LRP as compared to the naturally occurring RAP.

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In another preferred embodiment of the present invention, RAP is a fragment, mutant or analog. Preferably, the RAP fragment, mutant or analog retains LRP binding activity. More preferably, the RAP fragment, mutant or analog has increased affinity for LRP as compared to the naturally occurring RAP.

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In one embodiment, the RAP is a fragment having LRP binding activity. Such RAP fragments may comprise 10, 20, 30, 40, 50, 60, 75, 100, 125, 150, 175, 200, 250, 300 or 350 or more contiguous amino acids.

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In one embodiment, RAP comprises amino acids 1 to 357 of Figure 4 (full-length RAP; amino acids 1-19 to 323 of SEQ ID NO:4). RAP contains a signal sequence 34 amino acids in length. Thus, in another embodiment, RAP comprises amino acids 35 to 357 of Figure 4 (mature RAP; amino acids 1 to 323 of SEQ ID NO:4.).

25

In another embodiment of the present invention, RAP contains an N-terminal or a C-terminal deletion, or a combination of N- and C-terminal deletions. N-terminal deletions often result in a protein with increased stability. Thus, for example, deleting between 1 and 50 amino acids from the N-terminus of mature RAP is useful to produce a more stable RAP. Therefore, additional embodiments of the present invention include, for example, RAP comprising

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amino acids 36-357, 37-357, 38-357, 39-357, 40-357, 41-357, 42-357, 43-357, 44-357, 45-357, 46-357, 47-357, 48-357, 49-357, 50-357, 51-357, 52-357, 53-357, 54-357, 55-357, 56-357, 57-357, 58-357, 59-357, 60-357, 61-357, 62-357, 63-357, 64-357, 65-357, 66-357, 67-357, 68-357, 69-357, 70-357, 71-357, 72-357, 73-357, 74-357, 75-357, 76-357, 77-357, 78-357, 79-357, 80-357, 81-357,

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82-357, 83-357, 84-357 and 85-357 of Figure 4 (positions 1-323, 2-323, 3-323, 4-323, 5-323, 6-323, 7-323, 8-323, 9-323, 10-323, 11-323, 12-323, 13-323, 14-323, 15-323, 16-323, 17-323, 18-323, 19-323, 20-323, 21-323, 22-323, 23-323, 24-323, 25-323, 26-323, 27-323, 28-323, 29-323, 30-323, 31-323, 32-323, 33-323, 34-323, 35-323, 36-323, 37-323, 38-323, 39-323, 40-323, 41-323, 42-323,

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43-323, 44-323, 45-323, 46-323, 47-323, 48-323, 49-323 and 50-323 of SEQ ID NO:4).

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The LDL receptor binding domain encompasses amino acids 237 to 353 of Figure 4 (amino acids 203 to 319 of SEQ ID NO:4). Thus, a preferred embodiment of the present invention is RAP comprising amino acids 237 to 353 (amino acids 203 to 319 of SEQ ID NO:4).

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Another embodiment of the present invention is a polynucleotide encoding RAP.

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In another embodiment of the present invention, RAP or a polynucleotide encoding RAP is used to treat hemophilia either alone or in combination with a factor VIII mutant.

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Additional embodiments of the present invention include pharmaceutically acceptable compositions comprising RAP alone or in combination with one or more factor VIII mutants.

15 *Pharmaceutically Acceptable Compositions*

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Pharmaceutically acceptable compositions comprising mutant factor VIII or RAP, alone or in combination with appropriate pharmaceutical stabilization compounds, delivery vehicles, and/or carrier vehicles, are prepared according to known methods, as described in *Remington's Pharmaceutical Sciences* by E.W.

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Martin.

In one preferred embodiment, the preferred carriers or delivery vehicles for intravenous infusion are physiological saline or phosphate buffered saline.

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In another preferred embodiment, suitable stabilization compounds, delivery vehicles, and carrier vehicles include but are not limited to other human or animal proteins such as albumin.

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Phospholipid vesicles or liposomal suspensions are also preferred as pharmaceutically acceptable carriers or delivery vehicles. These can be prepared according to methods known to those skilled in the art and can contain, for example, phosphatidylserine/phosphatidylcholine or other compositions of

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10 phospholipids or detergents that together impart a negative charge to the surface, since factor VIII binds to negatively charged phospholipid membranes. 10

15 Liposomes may be prepared by dissolving appropriate lipid(s) (such as stearoyl phosphatidyl ethanolamine, stearoyl phosphatidyl choline, arachadoyl phosphatidyl choline, and cholesterol) in an inorganic solvent that is then evaporated, leaving behind a thin film of dried lipid on the surface of the container. An aqueous solution of the mutant factor VIII or RAP is then introduced into the container. The container is then swirled by hand to free lipid material from the sides of the container and to disperse lipid aggregates, thereby 20

20 forming the liposomal suspension.

25 Mutant factor VIII or RAP can be combined with other suitable stabilization compounds, delivery vehicles, and/or carrier vehicles, including vitamin K dependent clotting factors, tissue factor, and von Willebrand factor (vWF) or a fragment of vWF that contains the factor VIII binding site, and 30

35 polysaccharides such as sucrose.

30 Mutant factor VIII can be stored bound to vWF to increase the shelf-life of the mutant molecule. Additionally, lyophilization of factor VIII can improve the yield of active molecules in the presence of vWF. Lyophilization can also 35

40 factor VIII used by commercial suppliers can be employed for storage of mutant factor VIII or RAP. These methods include: (1) lyophilization of factor VIII in a partially-purified state (as a factor VIII "concentrate" that is infused without further purification); (2) immunoaffinity-purification of factor VIII by the Zimmerman method and lyophilization in the presence of albumin, which 45

45 stabilizes the factor VIII; (3) lyophilization of recombinant factor VIII in the presence of albumin.

50 Additionally, factor VIII has been indefinitely stable at 4°C in 0.6 M NaCl, 20 mM MES, and 5 mM CaCl₂ at pH 6.0 and also can be stored frozen in these buffers and thawed with minimal loss of activity.

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Methods of Treatment

Mutant factor VIII or RAP is used to treat uncontrolled bleeding due to factor VIII deficiency (e.g., intraarticular, intracranial, or gastrointestinal hemorrhage) in hemophiliacs with and without inhibitory antibodies and in patients with acquired factor VIII deficiency due to the development of inhibitory antibodies. The active materials are preferably administered intravenously.

Factor VIII is classically defined as that substance present in normal blood plasma that corrects the clotting defect in plasma derived from individuals with hemophilia A. The coagulant activity *in vitro* of purified and partially-purified forms of factor VIII is used to calculate the dose of factor VIII for infusions in human patients and is a reliable indicator of activity recovered from patient plasma and of correction of the *in vivo* bleeding defect. There are no reported discrepancies between standard assay of novel factor VIII molecules *in vitro* and their behavior in the dog infusion model or in human patients. according to Lusher, J. M., *et al.*, *New. Engl. J. Med.* 328:453-459 (1993); Pittman, D. D., *et al.*, *Blood* 79:389-397 (1992), and Brinkhous *et al.*, *Proc. Natl. Acad. Sci.* 82:8752-8755 (1985).

Usually, the desired plasma factor VIII level to be achieved in the patient through administration of the mutant factor VIII is in the range of 30-100% of normal. In a preferred mode of administration of the mutant factor VIII, the composition is given intravenously at a preferred dosage in the range from about 5 to 50 units/kg body weight, more preferably in a range of 10-50 units/kg body weight, and most preferably at a dosage of 20-40 units/kg body weight; the interval frequency is in the range from about 8 to 24 hours (in severely affected hemophiliacs); and the duration of treatment in days is in the range from 1 to 10 days or until the bleeding episode is resolved. See, e.g., Roberts, H. R., and M. R. Jones, "Hemophilia and Related Conditions – Congenital Deficiencies of Prothrombin (Factor II, Factor V, and Factors VII to XII)," Ch. 153, 1453-1474, 1460, in *Hematology*, Williams, W. J., *et al.*, ed. (1990).

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Administration of an effective amount of RAP will result in similar levels of factor VIII in patient blood as indicated above. Patients with inhibitors may require more mutant factor VIII, or patients may require less mutant factor VIII because of its higher specific activity than human factor VIII or increased plasma half-life. Likewise, patients may require more or less RAP, depending on RAP's binding affinity to LRP or other factor VIII clearance receptor, or depending on its stability in circulating blood. As in treatment with human or porcine factor VIII, the amount of mutant factor VIII or RAP infused is defined by the one-stage factor VIII coagulation assay and, in selected instances, *in vivo* recovery is determined by measuring the factor VIII in the patient's plasma after infusion. It is to be understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that the concentration ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition.

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Administration

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In a preferred embodiment, pharmaceutically acceptable compositions of mutant factor VIII or RAP alone or in combination with stabilizers, delivery vehicles, and/or carriers are infused into patients intravenously according to the same procedure that is used for infusion of human or animal factor VIII.

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The treatment dosages of mutant factor VIII or RAP composition that must be administered to a patient in need of such treatment will vary depending on the severity of the factor VIII deficiency. Generally, dosage level is adjusted in frequency, duration, and units in keeping with the severity and duration of each patient's bleeding episode. Accordingly, the mutant factor VIII or RAP is included in the pharmaceutically acceptable carrier, delivery vehicle, or stabilizer in an amount sufficient to deliver to a patient a therapeutically effective amount of the mutant protein to stop bleeding, as measured by standard clotting assays.

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Treatment can take the form of a single intravenous administration of the composition or periodic or continuous administration over an extended period of time, as required. Alternatively, mutant factor VIII or RAP can be administered subcutaneously or orally with liposomes in one or several doses at varying intervals of time. Mutant factor VIII or RAP can also be used to treat uncontrolled bleeding due to factor VIII deficiency in hemophiliacs who have developed antibodies to human factor VIII.

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Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the protein, which matrices are in the form of shaped articles, e.g. films, or microcapsules.

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Examples of sustained-release matrices include polyesters, hydrogels, e.g., poly(2-hydroxyethyl-methacrylate) as described by Langer *et al.*, *J. Biomed. Mater. Res.* 15:167-277 (1981) and Langer, *Chem. Tech.* 12: 98-105 (1982) or

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poly(vinylalcohol), polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, *Biopolymers* 22:547-556 (1983)), non-degradable ethylene-vinyl acetate (Langer *et al.*, *supra*), degradable lactic acid-glycolic acid copolymers such as the Lupron DepotTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid (EP 133,988).

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While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated proteins remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37 °C, resulting in a loss of biological activity and possible changes in

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immunogenicity. Rational strategies can be devised for protein stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization can be achieved by modifying sulphydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

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Sustained-release blood factor compositions also include liposomally entrapped blood factor or antibody. Liposomes containing the claimed blood factor or antibody are prepared by methods known per se: DE 3,218,121; Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688-3692 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese patent application 83-118008; U.S. Pat. No. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamellar type, the selected proportion being adjusted for the optimal blood factor therapy. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556. Additionally, Giles, A. R., *et al.* *Brit. J. Hematol.* 69:491-497 (1988) describe the formulation of factor Xa in phosphatidylcholine-phosphatidylserine vesicles.

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Additionally, mutant factor VIII or RAP can be administered by transplant of cells genetically engineered to produce the protein or by implantation of a device containing such cells, as described below.

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Gene Therapy

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Polynucleotides encoding the mutant factor VIII or RAP may be employed in accordance with the present invention by expression of such mutant factor VIII or RAP *in vivo*, in treatment modalities often referred to as "gene therapy."

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Mutant factor VIII or RAP can also be delivered by gene therapy in the same way that human factor VIII can be delivered, using delivery means such as retroviral vectors. This method consists of incorporation of factor VIII cDNA into human cells that are transplanted directly into a factor VIII deficient patient or that are placed in an implantable device, permeable to the factor VIII molecules but impermeable to cells, that is then transplanted. The preferred method will be retroviral-mediated gene transfer. In this method, an exogenous gene (e.g., a factor VIII cDNA) is cloned into the genome of a modified retrovirus. The gene/cDNA is inserted into the genome of the host cell by viral machinery where it will be expressed by the cell. The retroviral vector is modified so that it will

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not produce virus, preventing viral infection of the host. The general principles for this type of therapy are known to those skilled in the art and have been reviewed in the literature (e.g., Kohn, D.B., and P.W. Kantoff, *Transfusion* 29:812-820 (1989)).

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5 Thus, for example, cells from a patient may be engineered with a polynucleotide, such as a DNA or RNA, encoding a polypeptide *ex vivo*, and the engineered cells then can be provided to a patient to be treated with the polypeptide. For example, cells may be engineered *ex vivo* by the use of a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention. Such methods are well-known in the art and their use in the present invention will be apparent from the teachings herein.

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10 Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by procedures known in the art. For example, a polynucleotide of the invention may be engineered for expression in a replication defective retroviral vector, as discussed above. The retroviral expression construct then may be isolated and introduced into a packaging cell is transduced with a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention such that the packaging cell now produces infectious viral particles containing the gene of interest. These producer cells may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering a polypeptide of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention.

15 Retroviruses from which the retroviral plasmid vectors herein above mentioned may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, adenovirus, Myeloproliferative Sarcoma Virus, and mammary tumor virus. In one embodiment, the retroviral plasmid vector is derived from Moloney Murine Leukemia Virus.

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Such vectors will include one or more promoters for expressing the polypeptide. Suitable promoters which may be employed include, but are not limited to, the retroviral LTR; the SV40 promoter; and the human cytomegalovirus (CMV) promoter described in Miller *et al.*, *Biotechniques* 7: 980-990 (1989), or any other promoter (e.g., cellular promoters such as eukaryotic cellular promoters including, but not limited to, the histone, RNA polymerase III, and β -actin promoters). Other viral promoters which may be employed include, but are not limited to, adenovirus promoters, thymidine kinase (TK) promoters, and B19 parvovirus promoters. The selection of a suitable promoter will be apparent to those skilled in the art from the teachings contained herein.

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5 The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, Y-2, Y-AM, PA12, T19-14X, VT-19-17-H2, YCRE, YCRIP, GP+E-86, GP+envAm12, and DAN

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10 cell lines as described in Miller, A., *Human Gene Therapy* 1:5-14 (1990). The

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15 vector may be transduced into the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO_4 precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then 30 administered to a host.

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20 The producer cell line will generate infectious retroviral vector particles, which include the polynucleotide(s) encoding the polypeptides. Such retroviral vector particles then may be employed to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express the 40 polynucleotide(s) encoding the polypeptide. Eukaryotic cells which may be transduced include, but are not limited to, embryonic stem cells, embryonic 45 carcinoma cells, as well as hematopoietic stem cells, hepatocytes, fibroblasts, myoblasts, keratinocytes, endothelial cells, and bronchial epithelial cells.

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25 The following examples are illustrative only and are not intended to limit 50 the scope of the invention as defined by the appended claims. It will be apparent

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to those skilled in the art that various modifications and variations can be made in the methods of the present invention without departing from the spirit and scope of the invention. Thus, it is intended that the present invention cover the modifications and variations of this invention provided they come within the scope of the appended claims and their equivalents.

15

All patents, publications and publicly available sequences referred to herein are expressly incorporated by reference.

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Examples

Example 1

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10 Activated factor VIII (fVIIIa) functions in the intrinsic pathway of blood coagulation as a cofactor for factor IXa in the conversion of factor X to activated factor X (Xa). When IXa is bound to membrane and fVIII the rate of factor X to IXa conversion increases 100,000-1,000,000 fold. The procoagulant activity of fVIIIa is regulated by rapid and potentially reversible dissociation of the A2 subunit from the A1/A3C1C2 dimer and by activated protein C (APC) proteolysis of the residual fVIIIa. Removal of the A2 and A1/A3C1C2 fragments is an additional *in vivo* mechanism to control factor VIIIa activity at the site of blood coagulation.

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Activated factor VIII (fVIIIa) functions in the intrinsic pathway of blood coagulation as a cofactor for factor IXa in the conversion of factor X to activated factor X (Xa). When IXa is bound to membrane and fVIII the rate of factor X to IXa conversion increases 100,000-1,000,000 fold. The procoagulant activity of fVIIIa is regulated by rapid and potentially reversible dissociation of the A2 subunit from the A1/A3C1C2 dimer and by activated protein C (APC) proteolysis of the residual fVIIIa. Removal of the A2 and A1/A3C1C2 fragments is an additional *in vivo* mechanism to control factor VIIIa activity at the site of blood coagulation.

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We tested this in a model system using mouse embryonic fibroblasts (MEF) that express low density lipoprotein receptor related protein (LRP) a multi ligand endocytic receptor and PEA 13 fibroblasts that are genetically deficient in LRP. Using the above model system we studied the mechanisms of cellular uptake and degradation of thrombin activated fVIII subunits to evaluate the role of these mechanisms in regulation of fVIIIa level.

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Methods

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Cell mediated ligand internalization and degradation assays. Cells were seeded into 24 well dishes and allowed to grow for 24 hours at 37°C. 5% CO₂, MEF and PEA 13 cells were incubated for selected time intervals at 37°C with

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5 ¹²⁵I-labeled fVIIIa fragments in the presence and absence of unlabeled competitors as described in the figure legends. Radioactivity appearing in the cell culture medium that was soluble after precipitation with 10% trichloroacetic acid (TCA) was taken to represent degraded ligand. Total ligand degradation was corrected

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by subtracting the amount of 10% TCA soluble radioactivity occurred in control wells lacking cells. The amount of labeled ligand bound to the cell surface or that was internalized by cells was determined as follows. Cells were washed with cold phosphate buffered saline and treated with a trypsin EDTA proteinase K solution. Surface bound material was defined as the amount of radioactive ligand released by this treatment and the amount of internalized ligand was defined as

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10 the amount of radioactivity which remained associated with the cell pellet following the treatment.

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Determining of the A2 affinity for LRP. LRP (3.5 µg/ml) in 0.1 M NaHCO₃, pH 9.6 was incubated in Immulon I microtiter well strips for 16 hours at 4°C. After washing with TBS, 5 mM CaCl₂, 0.05% Tween 20 buffer (TBS-T) and blocking with 3% BSA, ¹²⁵I-A2 (5 nM) and increasing concentrations unlabeled A2 (0-1750 nM) were added. Following the incubation for 1 hour at 37°C and washing with TBS-T, the radioactivity bound to the wells was counted. ¹²⁵I-A2 binding in the presence of unlabeled A2 was plotted using the computer program "Ligand." The K_d value for A2/LRP binding was calculated from the displacement curve, showing a best fit of the data to a single class of sites.

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Effect of RAP on the clearance of ¹²⁵I-A2 domain from the plasma of mice. To elucidate the role of LRP receptor in the clearance of the A2 domain from

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plasma *in vivo* we tested the plasma level of ^{125}I -labeled A2 in the presence and
absence of RAP after tail vein injection in mice. 250 μl samples of A2 (36 nM),
in the presence and absence of RAP (267 μM) were injected into the tail vein of
BALB/c mice. At the indicated times, blood (50 μl) was collected into 10 μl of
0.5 M EDTA and counted for its ^{125}I content. RAP significantly delays the
plasma elimination of A2 domain. This experiment indicates that a RAP
dependent hepatic receptor, LRP, plays a major role in the removal of A2 from
circulation.

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LRP receptor mediated internalization and degradation of the ^{125}I -A2
domain by fibroblast cells. The cellular uptake and degradation of activated
factor VIII fragments was studied using mouse embryonic fibroblast (MEF) cells
expressing low density lipoprotein receptor - related protein (LRP), a multi ligand
endocytic receptor, and PEA 13 cells represents fibroblasts lacking LRP. The
fVIIIa subunits interaction with MEF and PEA 13 cells represent an adequate
model for *in vivo* processes because fibroblast cells became exposed to
coagulation site upon vascular injury. LRP mediated internalization and
degradation of some proteins (Thrombin:ATIII complex and other complexes of
thrombin with inhibitors, tissue factor pathway inhibitor involved in coagulation
cascade is known.

^{125}I -A2 (10 nM) was incubated with cells for several times and amount of
surface bound, internalized and degraded ^{125}I -labeled protein were determined as
described under "Methods." The A2 domain was internalized and degraded by
MEF cells but not by PEA 13 cells suggesting that expression of LRP receptor is
required for these processes. The internalization and degradation of A2 was
blocked by RAP, an inhibitor of LRP binding to its ligands.

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Internalization of the ^{125}I -A2 and APC cleaved A2 domain, by LRP
presenting MEF cells and control PEA 13 cells, lacking LRP. Inactivation of
fVIIIa by APC leads to a cleavage of the A2 at Arg⁵⁶². Since cofactor activity

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cannot be reconstituted from A2_N/A2_C and A1/A3C1C2 dimer, we proposed that A2_N/A2_C removal from circulation may occur by a mechanism different than that for intact A2. To examine the effect of proteolysis by APC on cellular internalization of the A2 domain, we compared the ¹²⁵I-A2 and ¹²⁵I-A2_N/A2_C uptake by MEF and PEA 13 cells. We found that in contrast to A2 domain, the internalization of ¹²⁵I-A2_N/A2_C is not mediated by LRP receptor.

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Binding the A2 domain to the immobilized LRP. To the microtiter wells with immobilized LRP ¹²⁵I-A2 (5 nM) and increasing concentrations of unlabeled A2 (0-1750 nM) were added. After incubation for 1 hour at 37°C the wells were washed with TBS-T and radioactivity bound to the wells was counted. ¹²⁵I-A2 binding in the presence of unlabeled A2 is expressed as the percentage of ¹²⁵I-A2 binding, when no competitor was added. The data was analyzed using the computer program "Ligand". The K_d value for A2/ LRP binding calculated from the displacement data was 130 nM.

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Internalization of ¹²⁵I-labeled A1/A3C1C2 and A1³³⁶/A3C1C2 by fibroblast cells. We proposed that phospholipid binding site previously localized to the C2 domain of fVIII light chain mediates the cellular surface binding and internalization of A1/A3C1C2 and A1³³⁶/A3C1C2 dimers. To test this hypothesis we determined internalization ¹²⁵I-A1/A3C1C2 and ¹²⁵I-A1³³⁶/A3C1C2 by MEF cells in the presence and absence of anti-C2 domain monoclonal antibody NMC-VIII/5, which blocks the membrane binding sites of the C2 domain.

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Wells containing 2x10⁵ MEF cells were incubated with 3 nM of ¹²⁵I-A1/A3C1C2 or 3 nM of ¹²⁵I-A1³³⁶/A3C1C2 at 37°C in the presence or absence of 30 nM monoclonal antibody NMC-VIII/5. In the control experiments, PEA 13 cells lacking LRP were incubated as above with ¹²⁵I-A1/A3C1C2 and ¹²⁵I-A1³³⁶/A3C1C2. At several times internalization of the dimers was described under "Methods."

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Since internalization of both ^{125}I -A1/A3C1C2 and ^{125}I -A1 336 /A3C1C2 dimers was completely inhibited by monoclonal antibody NMC-VIII/5, that recognizes the membrane binding site of fVIII C2 domain, we concluded that membrane binding of C2 is a critical step required for internalization of the above dimers. The rate of internalization was similar for MEF and PEA 13 cells, which indicates that LRP receptor is not involved in this process.

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Degradation of ^{125}I -A1/A3C1C2 and ^{125}I -A1 336 /A3C1C2 by MEF cells. MEF cells were incubated with ^{125}I -A1/A3C1C2 (3 nM) or ^{125}I -A1 336 /A3C1C2 (3 nM) for 22 hours at 37°C in the presence and absence PAP (1 μM). The degradation of dimers was measured as described under "Methods".

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The degradation of A1/A3C1C2 dimer is RAP dependent. In contrast, degradation of APC cleaved A1 336 /A3C1C2 dimer is RAP independent and does not correlate with LRP expression.

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Conclusions

15 The A2 domain was internalized and degraded by mouse embryonic fibroblasts (MEF) which are expressing low density lipoprotein receptor - related protein (LRP), a multi ligand endocytic receptor. The internalization and degradation of A2 was blocked by RAP, an inhibitor of LRP binding to its ligands. *In vivo* clearance studies in mice demonstrated that RAP inhibited the 20 clearance of ^{125}I -A2 from circulation. The radioactivity was preferentially 40 accumulated in liver in the absence but not in the presence of RAP. This indicates that a RAP sensitive hepatic receptor most likely LRP, plays a major role in the removal of ^{125}I -A2 from the circulation.

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25 The phospholipid binding site previously localized to the C2 domain of fVIII light chain mediates the cellular membrane binding and internalization of A1/A3C1C2 and A1 336 /A3C1C2 dimers.

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LRP receptor does not participate in cellular uptake and degradation of fragments A2_N/A2_C and A1³³⁶/A3C1C2, produced by irreversible inactivation of fVIIIa by APC. A2 and A1/A3C1C2 fragments produced by reversible inactivation of fVIIIa are removed by LRP-mediated and LRP-independent mechanisms, respectively. LRP is involved in the regulation of coagulation processes *in vivo*, by removal of A2 domain and A1/A3C1C2 dimer, the fragments from which active factor VIIIa can be reconstituted.

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Example 2

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The plasma glycoprotein factor VIII (fVIII) serves as a cofactor for the factor X activation complex in the intrinsic pathway of blood coagulation. FVIII circulates in plasma in a tight noncovalent complex with its carrier protein von Willebrand factor (vWF). Although the complex formation of fVIII with vWF is critical for maintenance of a normal half-life and level of fVIII in circulation, the mechanisms associated with fVIII turnover are not well defined. In the present study, we found that catabolism of fVIII is mediated by the low density lipoprotein receptor-related protein/α₂-macroglobulin receptor (LRP), a liver endocytic, receptor responsible for *in vivo* clearance of a number of structurally unrelated ligands. A specific binding between fVIII and LRP was demonstrated by homologous ligand competition experiments, where a K_d of 116 nM was determined for fVIII binding to LRP. A 39 kDa receptor-associated protein (RAP), an antagonist of ligand binding by LRP, completely inhibited fVIII binding to purified LRP. The region of fVIII involved in its binding to LRP was localized to the A2 domain residues 484-509, based on the ability of the isolated A2 domain and the synthetic A2 domain peptide 484-509 to prevent fVIII interaction with LRP. Since vWF did not inhibit fVIII binding to LRP, we proposed that LRP receptor may internalize fVIII from its complex with vWF. In agreement with this, mouse embryonic fibroblasts (MEF) that express LRP, but not fibroblasts genetically deficient in LRP (PEA 13), were able to internalize and

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10 degrade ^{125}I -fVIII/vWF complex. The latter processes were competed by RAP and A2 subunit of fVIII, indicating that cellular internalization and subsequent degradation were mediated by interaction of the A2 domain of fVIII with LRP. MEF cells were not able to internalize ^{125}I -vWF from ^{125}I -vWF /fVIII complex. 5 This indicates that vWF does not follow fVIII in the LRP-mediated pathway and dissociates from fVIII at the early stage of endocytosis. *In vivo* clearance studies of ^{125}I -fVIII/vWF complex in mice demonstrated that RAP prolonged the half-life of ^{125}I -fVIII in circulation by 2.5-fold, indicating that RAP-sensitive receptor, most likely LRP, is responsible for the plasma clearance of fVIII.

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10 ***Introduction***

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The plasma glycoprotein factor VIII (fVIII) functions as a cofactor for the factor X activation enzyme complex in the intrinsic pathway of blood coagulation, and it is decreased or nonfunctional in patients with hemophilia A. The fVIII protein consists of a homologous A and C domains and a unique B 30 15 domain which are arranged in the order A1-A2-B-A3-C1-C2 (Vehar, G.A., *et al.*, *Nature* 312:337-340 (1984)). It is processed to a series of Me^{2+} linked heterodimers produced by cleavage at the B-A3 junction (Fay, P. J., *et al.*, *Biochem. Biophys. Acta.* 871:268-278 (1986)), generating a light chain (LCh) 35 20 consisting of an acidic region (AR) and A3, C1, and C2 domains and a heavy chain (HCh) which consists of the A1, A2, and B domains (Fig. 1).

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Transplantational studies both in animals and in humans demonstrated that the liver hepatocytes are the major fVIII-producing cells (Lewis, J. H., *et al.*, *N. Engl. J. Med.* 312:1189-1191 (1985); Bontempo, F. A., *et al.*, *Blood* 69:1721-1724 (1987)). Immediately after release into circulation, fVIII binds with high 45 25 affinity ($K_d < 0.5$ nM (MacGregor, I.R., *et al.*, *Vox. Sang.* 69:319-327 (1995); Saenko, E.L. and Scandella, D., *J. Biol. Chem.* 272:18007-18014 (1995)) to its carrier protein vWF to form a tight, noncovalent complex, which is required for maintenance of a normal fVIII level in the circulation. Complex formation with

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vWF stabilizes association of the LCh and HCh within fVIII molecule (Wise, R.J., *et al.*, *J. Biol. Chem.* 266:21948-21955 (1991)) and prevents fVIII from C2-domain mediated binding to phospholipid membranes (Gilbert, G.E., *et al.*, *J. Biol. Chem.* 267:15861-15868 (1992)), activation by activated factor X (Koppelman, S.J., *et al.*, *J. Lab. Clin. Med.* 123:585-593 (1994)) and from protein C-catalyzed inactivation (Fay, P.J., *et al.*, *J. Biol. Chem.* 266:2172-2177 (1991)). vWF comprises a series of high molecular weight, disulfide-bonded multimers with molecular weight values as high as 2×10^7 Da (Hoyer, L.W. and Shainoff, J.R., *Blood* 55:1056-1059 (1980)) and circulates in plasma at 10 $\mu\text{g}/\text{ml}$ or 50 nM, assuming a molecular mass of 270 kDa for vWF monomers (Girma, J.-P., *et al.*, *Biochemistry* 25:3156-3163 (1986)). Since the concentration of fVIII in plasma is approximately 1 nM (Wion, K., *et al.*, *Nature* 317:726-730 (1985)), one fVIII molecule is bound per 50 vWF monomers (Vlot, A.J., *et al.*, *Blood* 85:3150-3157 (1995)).

Activation of fVIII by thrombin leads to dissociation of activated fVIII (fVIIIa) from vWF and to at least 100-fold increase of the cofactor activity. The fVIIIa is a A1/A2/A3-C1-C2 heterotrimer (Fay, P.J., *et al.*, *J. Biol. Chem.* 266:8957-8962 (1991)) in which domains A1 and A3 retain the metal ion linkage (Fig. 1) and the stable dimer A1/A3-C1-C2 is weakly associated with the A2 subunit through electrostatic forces (Fay, P.J., *et al.*, *J. Biol. Chem.* 266:8957-8962 (1991)). Spontaneous dissociation of the A2 subunit from the heterotrimer results in non-proteolytic inactivation of fVIIIa.

Infusion of fVIII/vWF complex or purified plasma or recombinant fVIII into patients with severe hemophilia A who do not have fVIII (Fijnvandraat, K., *et al.*, *Thromb. Haemostas.* 77:298-302 (1997); Morfini, M., *et al.*, *Thromb. Haemostas.* 68:433-435 (1992)) or in normal individuals (Over, J., *et al.*, *J. Clin. Invest.* 62:223-234 (1978)) results in a similar fVIII disappearance with a half-life of 12-14 hours. Although the complex between fVIII and vWF is crucial for normal half-life and level of fVIII in the circulation, the mechanisms associated with turnover of fVIII/vWF complex are not well defined. We proposed that

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10 fVIII/vWF complex is eliminated from plasma via clearance receptor and tested
the possibility that this receptor is low density lipoprotein related protein receptor
15 (LRP). Cellular endocytosis mediated by LRP was shown to be a mechanism of
removal of a number of structurally unrelated ligands including several proteins
5 related to coagulation or fibrilolysis. These ligands are: complexes of thrombin
with antithrombin III (ATIII), heparin cofactor II (HCII) (Kounnas, M.Z., *et al.*,
J. Biol. Chem. 271:6523-6529 (1996)), protease nexin I (Knauer, M.F., *et al.*, J.
Biol. Chem. 272:12261-12264 (1997)), complexes of urokinase-type and tissue-
type plasminogen activators (u-PA and t-PA, respectively) with plasminogen
20 activator inhibitor (PAI-1) (Nykjaer, A., *et al.*, J. Biol. Chem. 267:14543-14546
(1992); Orth, K., *et al.*, Proc. Natl. Acad. Sci. 89:7422-7426 (1992)),
thrombospondin (Mikhailenko, I., *et al.*, J. Biol. Chem. 272:6784-6791 (1997)),
25 tissue factor pathway inhibitor (TFPI) (Warshawsky, I., *et al.*, Proc. Natl. Acad.
Sci. 91:6664-6668 (1994)), and factor Xa (Narita, M., *et al.*, Blood 91:555-560
15 (1998); Ho, G., *et al.*, J. Biol. Chem. 271:9497-9502 (1996)).

30 LRP, a large cell-surface glycoprotein identical to α_2 -macroglobulin
receptor (Strickland, D.K., *et al.*, J. Biol. Chem. 265:17401-17404 (1990)), is a
member of the low density lipoprotein (LDL) receptor family which also includes
35 the LDL receptor, very low density lipoprotein (VLDL) receptor, vitellogenin
receptor and glycoprotein 330 receptor. LRP receptor consists of the non-
covalently linked 515 kDa α -chain (Herz, J., *et al.*, EMBO J. 7:4119-4127 (1988))
containing binding sites for LRP ligands, and the 85 kDa transmembrane β -chain.
Within the α -chain, cluster of cysteine-rich class A repeats is responsible for
40 ligand binding (Moestrup, S. K., *et al.*, J. Biol. Chem. 268:13691-13696 (1993)).
25 In contrast to the acidic ligand binding region in LRP, its ligands expose regions
rich in positively charged amino acid residues (Moestrup, S.K., *Biochim. Biophys.
Acta* 1197:197-213 (1994)). This type of binding and 31 class A repeats present
45 in LRP may be responsible for its wide ligand diversity and ability to serve as a
multi-ligand clearance receptor. LRP is expressed in many cell types and tissues
30 including placenta, lung and brain (Moestrup, S.K., *et al.*, *Cell Tissue Res.*
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269:375-382 (1992)) and is a major endocytic receptor in the liver (Strickland, D.K., *et al.*, *FASEB J.* 9:890-898 (1995)). A 39 kDa receptor-associated protein (RAP) binds to LRP with high affinity ($K_d=4$ nM (27)) and inhibits binding and LRP-mediated internalization and degradation of all ligands (Moestrup, S.K. *Biochim. Biophys. Acta* 1197:197-213 (1994); Williams, S.E., *et al.*, *J. Biol. Chem.* 267:9035-9040 (1992)), therefore serving as a useful tool for testing whether LRP is involved in endocytosis of a given ligand.

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20 In the present study we demonstrated that fVIII specifically binds to LRP, and that LRP mediates the internalization and subsequent degradation of fVIII in cultured fibroblasts and appears to be responsible for *in vivo* clearance of fVIII from circulation. We also demonstrated that interaction of the A2 domain of fVIII with LRP is responsible for mediating catabolism of fVIII.

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Experimental Procedures

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35 **Monoclonal Antibodies.** The monoclonal antibodies (mAbs) C4 (epitope within the fVIII light chain residues 1670-1684 (Foster, P.A., *et al.*, *J. Biol. Chem.* 263:5230-5234 (1988))), C5 (epitope within A1 residues 351-361) and T5 (epitope within the residues 701-740 (Fulcher, C.A., *et al.*, *J. Clin. Invest.* 76:117-124 (1985))) were kindly provided by Dr. Carol Fulcher (Scripps Clinic and Research Foundation, La Jolla, CA). The anti-A2 mAb 8860 was generously provided by Baxter/Hyland. Mah 413 (epitope within A2 domain residues 484-509 (Healey, *et al.*, *J. Biol. Chem.* 270:14505-14509 (1995))) was prepared as described previously (Saenko, E.L., *et al.*, *J. Biol. Chem.* 269:11601-11605 (1994)).

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45 **Proteins.** LRP was isolated from human placenta as described (Ashcom, J.D., *et al.*, *J. Cell Biol.* 110:1041-1048 (1990)). Human RAP was expressed in bacteria and purified as described (Williams, S.E., *et al.*, *J. Biol. Chem.* 267:9035-9040 (1992)). FVIII was purified from therapeutic concentrates of

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Method M, American Red Cross (Saenko, E.L., *et al.*, *J. Biol. Chem.* 271:27424-27431 (1996)). HCh and LCh were prepared from fVIII as described previously (Saenko, E.L. and Scandella, D., *J. Biol. Chem.* 272, 18007-18014 (1995)). Purification of the A1/A3-C1-C2 dimer and A2 subunit was performed using ion exchange chromatography of thrombin activated fVIII on a Resource S column (Pharmacia) (Fay, P.T., *et al.*, *J. Biol. Chem.* 268, 17861-17866 (1993)). Residual A2 present in the A1/A3-C1-C2 preparation was removed by its passage over an immobilized mAb 8860 column equilibrated in 20 mM Tris, pH 7.4, 0.15 M NaCl, 5 mM CaCl₂.

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10 **Radiolabeling of fVIII and synthetic peptides.** Prior to iodination fVIII and A2 were dialyzed into 0.2 M sodium acetate, 5 mM calcium nitrate, pH 6.8 (iodination buffer). Five µg of fVIII in 30 µl of iodination buffer were added to lactoperoxidase beads (Worthington Biochemical Corp.), 5 µl of Na¹²⁵I (100 mCi/ml, Amersham), and 5 µl of 0.03% H₂O₂ (Mallinckrodt) and incubated for 4 min. Free Na¹²⁵I was removed by chromatography on a PD10 column (Pharmacia). The specific radioactivity of fVIII and A2 was 3.5-5 µCi/µg of protein. The activity of ¹²⁵I-fVIII determined in the one-stage clotting assay (3740 units/µg) was similar to that of unlabeled fVIII.

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15 **Solid-phase binding assays.** Homologous and heterologous ligand displacement assays were performed as previously described (Williams, S.E., *et al.*, *J. Biol. Chem.* 267:9035-9040 (1992)). Microtiter wells were coated with purified LRP or BSA (3 µg/ml) in 50 mM Tr-is, 0.15 M NaCl, pH 8.0, for 16 h and then blocked with 3 % BSA in TBS. Coated wells were incubated with ¹²⁵I-A2 or ¹²⁵I-fVIII in 20 mM Tris-buffered saline pH 7.4, containing 5 mM CaCl₂, 0.05 % Tween-20 in the presence or absence of unlabeled competitors for 1 h at 37°C. The radioactivity bound to the wells was counted using a γ-counter (Pharmacia). Affinity constants were derived from homologous and heterologous displacement

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data using the computer program LIGAND (Munson, PT and Rodbard, D. *Anal. Biochem.* 107:220-239 (1980)).

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Cell-mediated ligand internalization and degradation assays. A normal mouse embryonic fibroblast line (MEF) and a mouse embryonic fibroblast cell line that is genetically deficient in LRP biosynthesis (PEA 13) were obtained from Dr. Joachim Herz (University of Texas Southwestern Medical Center, Dallas, TX) and maintained as described (Willnow, T.E. and Herz, J., *J. Cell Sci.* 107:719-726 (1994)). Cells were seeded at 1x10⁵ cells/well and allowed to grow for 24 h at 37°C, 5% CO₂. Cellular internalization and degradation assays were conducted as described previously (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 270:9307-9312 (1995)). Internalization and degradation of the ¹²⁵I-labeled fVIII and A2 was measured after incubation for indicated time intervals at 37°C in 0.5 ml of Dulbecco's modified medium (Gibco BRL) containing 2% BSA. Internalization was defined as radioactivity that is resistant to release from cells by trypsin (50 µg/ml) and proteinase K (50 µg/ml) (Sigma) in a buffer containing 5 mM EDTA. This treatment was previously shown to release radioligand bound to cell surface (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 270:9307-9312 (1995)) and therefore the ligand remained associated with cells after this treatment was considered as internalized. Degradation was defined as radioactivity in the medium that is soluble in 10% trichloroacetic acid. The value of degradation was corrected for non-cellular mediated degradation by subtracting the amount of degradation products generated in parallel wells lacking cells.

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Clearance of ¹²⁵I-A2 domain and ¹²⁵I-fVIII/vWF complex from mouse plasma. The complex of ¹²⁵I-labeled fVIII with vWF in the presence or absence of RAP (in a total volume 250 µl) was injected in a tail vein of BALB/C mice over a period of approximately 20 seconds. At selected time intervals following injection (1, 3, 6, and 18 min), blood (50 µl) was withdrawn from the orbital plexus into 10 µl of 100 mM EDTA, and the radioactivity of the aliquot was determined. The

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percentage of ligand remaining in circulation was calculated considering
radioactivity of the aliquot taken at 1 min after injection as 100%. The clearance
of each preparation was examined in two mice and the results were averaged. At
the end of experiment, animals were sacrificed, liver lobules and kidneys were
excised and weighed, followed by measuring the radioactivity in these tissues.

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Results

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Factor VIII binds to LRP and its binding is prevented by RAP. The ability
of fVIII to bind to LRP *in vitro* was examined in homologous displacement
binding assay. In the assay, binding of ^{125}I -fVIII (1 nM) to purified LRP, but not
to BSA-coated wells, was competed (> 90%) by excess of unlabeled fVIII (Fig.
5A). The quantitative data regarding fVIII interaction with LRP were derived
from the homologous displacement of ^{125}I -fVIII by unlabeled fVIII, which was
adequately described by a model containing a single class of fVIII binding sites
with K_d of 116 nM. To elucidate whether fVIII in a complex with vWF is also
able to bind to LRP, we tested the effect of vWF on ^{125}I -fVIII binding to
immobilized LRP. In this experiment, ^{125}I -fVIII was preincubated with vWF for
30 min at 37°C to allow complex formation prior to its addition to LRP coated
wells. As shown in Fig. 5A, ^{125}I -fVIII binding to LRP was not inhibited by vWF
up to the concentration of 1000 nM, which is 20-fold higher than its concentration
in plasma (50 mM (Vlot, A.J., *et al.*, *Blood* 85:3150-3157 (1995))). This
indicates that the complex formation with vWF does not affect fVIII ability to
bind to LRP.

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RAP, the antagonist of LRP-ligand binding, completely inhibited the
binding of ^{125}I -fVIII to LRP-coated wells with K_i of 2.5 nM (Fig. 5B), a value
similar to the previously determined affinity (4 nM) of RAP for LRP (Strickland,
D.K., *et al.*, *J. Biol. Chem.* 265:17401-17404 (1990)). Together, these results
demonstrate specific fVIII binding to LRP.

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The amino acid residues 484-509 within the fVIII A2 domain are responsible for fVIII binding to purified LRP. In order to localize fVIII region(s) involved in interaction with LRP, binding between ^{125}I -fVIII and immobilized LRP was competed by unlabeled fVIII fragments. As shown in Fig. 6, HCh and A2 domain of fVIII, but not LCh (AR-A3-C1-C2) or Al/A3-C1-C2 dimer, displaced ^{125}I -fVIII from LRP in the heterologous ligand displacement assay. The K_i values determined for the HCh and A2 were similar, 120 nM and 132 nM, respectively. The similarity of the above K_d value for fVIII binding to LRP and the K_i value for inhibition of this binding by isolated A2 subunit indicates that A2 domain of HCh is responsible for fVIII binding to LRP.

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To localize the region of the A2 domain responsible for the interaction with LRP, we tested the effect of anti-A2 monoclonal antibodies with known epitopes on fVIII/LRP binding. Fig. 7A shows that mAb 413 (epitope within the A2 domain residues 484-509 (Healey, J.F., *et al.*, *J. Biol. Chem.* 270:14505-14509 (1995))) but not mAb T5 (epitope within the A2 domain residues 701-740 (35)) is able to block fVIII/LRP interaction. The concentration of mAb 413 required for 50% inhibition of ^{125}I -fVIII/LRP binding was 2.5 nM. The low molar excess (2.5-fold) of mAb 413 over fVIII required for 50% inhibition of fVIII/LRP binding is consistent with a previously reported high affinity of mAb 413 for fVIII (Lollar, P., *et al.*, *J. Clin. Invest.* 93:2497-2504 (1994)). In a control experiment, mAbs C5 (epitope within Al residues 351-361) and C4 (epitope within LCh residues 1670-1684 (Foster, P.A., *et al.*, *J. Biol. Chem.* 263:5230-5234 (1988))) did not have any effect on fVIII binding to LRP (data not shown), which is consistent with the lack of participation of Al and LCh in fVIII binding to LRP.

Since it was previously demonstrated that mAb 413 recognizes synthetic peptide with a human fVIII sequence 484-509 (Healey, J.F., *et al.*, *J. Biol. Chem.* 270:14505-14509 (1995)), we tested if the region of the A2 domain encompassed by peptide 484-509 is involved in binding to LRP. As seen from Fig. 7B, the synthetic peptide 484-509, but not the control A2 peptide 432-456, inhibited fVIII binding to LRP in a dose-dependent fashion, indicating that the region 484-509

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of the A2 domain contains critical residues for fVIII binding to LRP. In a control experiment, no binding of ^{125}I -fVIII to BSA-coated wells was observed in the presence of peptide 484-509 (Fig. 7B).

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Internalization and degradation of ^{125}I -fVIII complex with vWF by cultured fibroblasts is mediated by LRP. Since the data presented above demonstrated specific interaction between fVIII and LRP, and vWF does not interfere with this interaction, we hypothesized that LRP may be also capable of mediating the cellular internalization of ^{125}I -fVIII from its complex with vWF. To examine this hypothesis, cellular uptake and degradation experiments were conducted in mouse embryonal fibroblasts (MEF) which express LRP and in PEA 13 fibroblasts that are genetically deficient in LRP (Willnow, T.E. and Herz, J. J. *Cell Sci.* 107:719-726 (1994)). The ^{125}I -fVIII/vWF complex was prepared by 30 min (37°C) incubation of ^{125}I -fVIII with vWF at their plasma concentrations of 1 nM and 50 nM, respectively. As shown in Figs. 8A and B, MEF cells, but not PEA 13 cells lacking LRP, were capable of internalizing and degrading of ^{125}I -fVIII in the presence of vWF. Further, internalization and degradation of ^{125}I -fVIII by MEF but not by PEA 13 fibroblasts was inhibited by RAP, an antagonist of ligand binding to LRP. The ability of RAP to block the uptake and degradation of ^{125}I -fVIII/vWF in MEF cells and inability of PEA 13 cells to efficiently mediate uptake and degradation indicates that LRP is the mediator of ^{125}I -fVIII/vWF catabolism. To further characterize the degradation pathway of fVIII in the MEF cells, we tested the effect of chloroquine (an agent that blocks lysosomal degradation) on ^{125}I -fVIII degradation. As seen from Fig. 8B, the degradation of ^{125}I -fVIII is completely inhibited by chloroquine.

25 To elucidate if fVIII internalization in the absence of vWF is also mediated by LRP, we measured the internalization and degradation of isolated ^{125}I -fVIII (Fig. 9). As seen from Figs. 9A and B, both internalization and degradation of isolated ^{125}I -fVIII by MEF fibroblasts is approximately 2-fold higher than that in the presence of vWF. RAP inhibited internalization and degradation of ^{125}I -fVIII

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to a lesser degree than those of ^{125}I -fVIII/vWF complex and, in addition, LRP-deficient PEA 13 fibroblasts were able to internalize and degrade isolated ^{125}I -fVIII. This indicates that LRP-mediated pathway is not the sole mechanism of fVIII internalization and degradation in the absence of vWF.

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5 To determine whether vWF bound to fVIII is also internalized and degraded by MEF cells, internalization and degradation of ^{125}I -labeled vWF complexed with fVIII was measured. As shown in Figs. 9A and B, the amounts of internalized and degraded ^{125}I -vWF by both MEF and PEA 13 cells were less than 5 % of the corresponding amounts of ^{125}I -fVIII catabolized from its complex with vWF under the same experimental conditions. This indicates that vWF does not follow fVIII in the LRP-mediated pathway and possibly dissociates from fVIII at early stage of endocytosis, prior to entry of the complex into endosomal compartments.

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30 The A2 subunit of fVIII inhibits endocytosis and degradation of ^{125}I -fVIII/vWF by MEF cells. Since we have demonstrated above that the A2 subunit of fVIII prevents an *in vitro* interaction between LRP and fVIII, we examined if A2 can also inhibit LRP-mediated internalization and degradation of fVIII/vWF complex by MEF cells. Figs. 10A and B demonstrate that 1000-fold excess of the A2 subunit over ^{125}I -fVIII/vWF complex effectively inhibit internalization (by >70% after 4 hours) and degradation (by >60% after 4 hours) of this complex. In contrast, A1/A3-C1-C2 heterodimer, which did not inhibit fVIII interaction with purified LRP in the above experiments, did not have any effect on ^{125}I -fVIII endocytosis and degradation by MEF cells (Fig. 10).

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45 To confirm that the inhibitory effect of the A2 subunit results from its direct competition with ^{125}I -fVIII/vWF complex for LRP-mediated internalization and degradation, we tested whether MEF cells are able to internalize and degrade isolated A2 subunit. As shown in Figs. 11A and B, ^{125}I -A2 is readily internalized and degraded by LRP-expressing MEF cells. Both the internalization and degradation of the ^{125}I -labeled A2 were blocked in the presence of RAP. In

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contrast, LRP-deficient PEA 13 cells were unable to internalize or degrade ^{125}I -A2 (Fig. 11), confirming that catabolism of the A2 subunit is LRP-mediated.

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To verify that LRP-mediated internalization and degradation of the A2 domain was not the unique feature of the MEF cells, we tested ^{125}I -labeled A2 internalization and degradation by smooth muscle cells (SMC) and alveolar epithelial cells (T2), which also express LRP on their surfaces (Moestrup, S.K., *Cell Tissue Res.* 269:375-382 (1992)). As shown in Figs. 11C and D, RAP effectively inhibited both internalization of ^{125}I -A2 by SMC and T2 (by 81 % and 64 %, respectively), and its degradation (by 78 % and 68 %), indicating that these processes were mediated by LRP.

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Thus, the data shown in Figs. 10 and 11 demonstrate that LRP is capable of binding fVIII via its A2 domain and of mediating fVIII endocytosis leading to lysosomal degradation.

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Effect of RAP on the plasma clearance of ^{125}I -fVIII and ^{125}I -A2. To determine whether LRP is capable of catabolizing the isolated fVIII A2 subunit and whole fVIII from its complex with vWF *in vivo*, the effect of RAP on the clearance rates of ^{125}I -fVIII/vWF complex and ^{125}I -A2 in mice was tested. As shown in Fig. 12A, RAP increased the half-life of both ^{125}I -A2 and ^{125}I -fVIII in mouse plasma by approximately 4 and 2.5-fold, respectively. In addition, in the absence of RAP, most of radioactivity was found in the liver but not in kidney, consistent with LRP presence in high abundance in hepatic tissues (Strickland, D.K., *et al.*, *FASEB J.* 9:890-898 (1995)). Thus, our data indicate that a RAP-sensitive hepatic receptor, LRP, plays a major role in the removal of fVIII and its A2 subunit from circulation.

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Discussion

10 In the present study we demonstrated that LRP mediates the internalization and degradation of human fVIII in a model system using LRP-expressing cells and is responsible for fVIII clearance *in vivo*. This conclusion
15 is based on several independent observations. First of all, we found that fVIII directly binds to purified LRP immobilized on microtiter wells, and that this binding is competed by RAP, an antagonist of ligands binding to LRP. Second,
20 ^{125}I -fVIII is internalized from its complex with vWF by mouse fibroblasts expressing LRP (MEF cells), but not by mouse fibroblasts genetically deficient in LRP (PEA 13 cells). Third, we demonstrated that RAP effectively inhibited the cellular uptake and degradation of ^{125}I -fVIII from its complex with vWF by MEF cells and *in vivo* clearance of ^{125}I -fVIII from circulation in mice.
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 Our studies revealed that the A2 domain of fVIII is responsible for its interaction with LRP, since only A2 domain and HCh, which contains the A2 domain, were able to inhibit the interaction of ^{125}I -fVIII with LRP in a purified system. Thus, it was concluded that A2 is responsible for fVIII binding to LRP. Based on the observation that vWF did not inhibit fVIII binding to LRP, we proposed that LRP may internalize fVIII from its complex with vWF. Indeed, mouse embryonic fibroblasts (MEF) that express LRP, but not fibroblasts genetically deficient in LRP, were able to internalize and degrade ^{125}I -fVIII in the presence of vWF. These processes were competed by RAP and A2 subunit of fVIII, indicating that cellular internalization and degradation were mediated by interaction of the A2 domain of fVIII with LRP. The physiological relevance of the observations utilizing the LRP-expressing cell model system was supported by *in vivo* clearance studies of ^{125}I -fVIII/vWF complex in mice which demonstrated that RAP prolonged the half-life of ^{125}I -fVIII in circulation by 2.5-fold, indicating that a RAP-sensitive receptor, most likely LRP, is responsible for the clearance of fVIII from plasma.
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Further localization of the region within the A2 domain responsible for its binding to purified LRP was initiated by the finding that monoclonal antibody with an epitope within A2 domain residues 484-509 completely inhibited fVIII interaction with LRP. Inhibition of fVIII/LRP binding by synthetic peptide with a human fVIII sequence 484-509 indicated that the region of the A2 domain is likely to be directly involved in fVIII binding to purified LRP.

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The region 484-509 contains 6 positively charged residues, Lys at positions 493, 496 and 499 and Arg at positions 484, 489 and 490. Basic residues in lipoprotein lipase (Chappell, D.A., *et al.*, *J. Biol. Chem.* 268:14168-14175 (1993)), u-PA/PAI-1 complex (Rodenburg, K.W., *et al.*, *Biochem. J.* 329:55-63 (1998)), and α_2 -macroglobulin (Howard, G.C., *et al.*, *J. Biol. Chem.* 271:14105-14111 (1996)) were previously shown to be critical for electrostatic interaction with LRP. Alanine substitution of the basic amino acid residues in lipoprotein lipase (Williams, S.E., *et al.*, *J. Biol. Chem.* 269:8653-8658 (1994)), u-PA/PAI-1 complex (Rodenburg, K.W., *et al.*, *Biochem. J.* 329:55-63 (1998)) and in the receptor binding fragment from α_2 -macroglobulin (Howard, G.C., *et al.*, *J. Biol. Chem.* 271:14105-14111 (1996)) lead to a considerable reduction of affinity for ligand binding to LRP and partial (Rodenburg, K.W., *et al.*, *Biochem. J.* 329:55-63 (1998)) or complete (Howard, G.C., *et al.*, *J. Biol. Chem.* 271:14105-14111 (1996)) inhibition of internalization and degradation of the mutants. Therefore, Ala or other amino acid substitutions within the 484-509 region of the recombinant fVIII are useful for reduction of the rate of its LRP-mediated endocytosis and generation of the fVIII mutants with a longer life in the circulation.

25 FVIII binds to purified LRP with affinity 116 nM, which is much lower than the concentration of fVIII/vWF complex in plasma (1 nM; Wion, K., *et al.*, *Nature* 317:726-730 (1985)). FVIII affinity for LRP is similar to that of the complexes of serine proteases with inhibitors such as ATIII/thrombin (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 271:6523-6529 (1996)), HCII/thrombin and α_1 -antitrypsin/trypsin (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 271:6523-6529 (1996)).

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which also bind to LRP with affinities 80-120 nM, and weaker than measured for other LRP ligands. It was shown (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 271:6523-6529 (1996)) that internalization and degradation of the above low affinity LRP ligands at their 1 nM concentration by MEF cells occur at a lower rate than that of the u-PA/PAI-1 complex which binds to LRP with high affinity ($K_d < 1$ nM). Therefore, relatively low affinity of fVIII for LRP is responsible for a slow rate of fVIII internalization and degradation by MEF cells, which is comparable to the rate of ATIII/thrombin, HCII/thrombin and α -1-antitrypsin/trypsin degradation at 1 nM concentration of each ligand. The low affinity of fVIII for LRP may also be a necessary requirement for the relatively long fVIII half-life (12-14 h) in plasma of normal individuals (Over, J., *et al.*, *J. Clin. Invest.* 62:223-234 (1978)). Alternatively, the low fVIII affinity for LRP may be compensated by concentration of fVIII molecules on the membrane of LRP-expressing cells, for example, via interaction with cell-surface proteoglycans which have been shown to facilitate the uptake of a number of LRP ligands including lipoprotein lipase (Chappell, D.A., *et al.*, *J. Biol. Chem.* 268:14168-14175 (1993)), hepatic lipase (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 270:9307-9312 (1995)), and thrombospondin (Mikhailenko, I., *et al.*, *J. Biol. Chem.* 270:9543-9549 (1995); Mikhailenko, I., *et al.*, *J. Biol. Chem.* 272:6784-6791 (1997)).

We found that internalization and degradation of isolated fVIII by MEF cells was greater than the corresponding processes for fVIII bound to vWF. In addition, catabolism of the isolated fVIII by MEF cells was only partially inhibited by RAP, indicating that LRP-mediated endocytosis of fVIII is not the sole mechanism of fVIII clearance in the absence of vWF. Our data suggest that in the presence of vWF, which blocks C2 domain-mediated fVIII binding to phospholipid membranes (Saenko, E.L. and Scandella, D., *J. Biol. Chem.* 270:13826-13833 (1995)), fVIII binds only to LRP, whereas in the absence of vWF, fVIII binds both to LRP and to an unidentified cell membrane component. The latter binding may lead to fVIII internalization via RAP-independent

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pathway, which may be mediated by unidentified receptor as it was previously proposed for hepatic lipase (Kounnas, M.Z., *et al.*, *J. Biol. Chem.* 270:9307-9312 (1995)). Since we found that ^{125}I -vWF is not internalized by MEF cells, we propose the model for fVIII endocytosis where fVIII/vWF complex binds to LRP and then vWF dissociates from fVIII during the early stage of fVIII endocytosis, *i.e.* during formation of the coated pits. Since the half-life for the dissociation of fVIII/vWF complex is about 1 hour (Saenko, E.L. and Scandella, D., *J. Biol. Chem.* 272, 18007-18014 (1995)), vWF may delay LRP-mediated endocytosis of fVIII according to the proposed model.

10 Faster catabolism of fVIII in the absence of vWF is consistent with a demonstrated shorter half-life of fVIII in patients with severe von Willebrand disease (vWD) lacking plasma vWF than that in hemophilia A patients, who have normal levels of vWF (Morfini, M., *et al.*, *Thromb. Haemostas.* 70:270-272 (1993); Lethagen, S., *et al.*, *Ann. Hematol.* 65:253-259 (1992)). Moreover, the 15 half-life of fVIII in vWD patients was prolonged by the presence of vWF in the infused fVIII preparation (Lethagen, S., *et al.*, *Ann. Hematol.* 65:253-259 (1992)). The above observations were previously explained by vWF-mediated stabilization 20 of fVIII by binding to vWF (Wise, R.J., *et al.*, *J. Biol. Chem.* 266:21948-21955 (1991)) and via secondary vWF-mediated release of endogenous fVIII (Wise, R.J., *et al.*, *J. Biol. Chem.* 266:21948-21955 (1991); Kaufman, R.J., *Mol. Cell. Biol.* 9:1233-1242 (1989)). Our data suggest that in addition to the above effects, vWF 25 may reduce the rate of fVIII clearance by preventing LRP-independent pathway and limiting fVIII clearance to LRP-mediated pathway.

30 The activity of the factor X activation complex (factor Xase), consisting 35 of membrane-bound activated fVIIa and factor IXa, can be down regulated by inactivation of fVIIa. The latter occurs via proteolytic degradation of fVIIa by activated protein C, factor Xa and factor IXa, and via spontaneous but reversible 40 dissociation of the A2 subunit from fVIIa heterotrimer (Fay, P. J. and Smudzin, T. M., *J. Biol. Chem.* 267:13246-13250 (1992)). Dissociation of the fVIIa 45 heterotrimer may be accelerated by LRP mediated internalization of the A2 50

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domain, and therefore complement regulation of fVIIIa activity at the sites of coagulation. This hypothesis is supported by availability of LRP at these sites, since LRP is exposed on the surface of monocytes and macrophage (Moestrup, S.K., *et al.*, *Exp. Cell. Res.* 190:195-203 (1990); Moestrup, S.K., *et al.*, *Cell Tissue Res.* 269:375-382 (1992)) and upon vascular injury on fibroblasts and smooth muscle cells (Moestrup, S.K., *et al.*, *Cell Tissue Res.* 269:375-382 (1992)). In addition, it was recently shown that isolated A2 but not isolated A1 and A3-C1-C2 subunits of activated fVIII is able to accelerate factor IXa-catalyzed conversion of factor X by approximately 100-fold (Fay, P.J. and Koshiba, K., *Blood* 92:353a (abstract) (1998)). Even though acceleration of the factor X activation by A2 is only 1 % of that in the presence of heterotrimeric activated fVIII (A1/A2/A3-C1-C2) (Fay, P.J. and Koshiba, K., *Blood* 92:353a (abstract) (1998)), it is possible that LRP-mediated removal of the A2, dissociated from fVIIIa bound to a phospholipid membrane at the site of coagulation, is important to prevent activation of factor X not in the place of the coagulation event.

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10 Even though acceleration of the factor X activation by A2 is only 1 % of that in the presence of heterotrimeric activated fVIII (A1/A2/A3-C1-C2) (Fay, P.J. and Koshiba, K., *Blood* 92:353a (abstract) (1998)), it is possible that LRP-mediated removal of the A2, dissociated from fVIIIa bound to a phospholipid membrane at the site of coagulation, is important to prevent activation of factor X not in the place of the coagulation event.

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15 In summary, the current study demonstrates that LRP can bind fVIII/vWF complex and mediate uptake of fVIII from it. *In vivo* clearance studies underscored the likelihood that LRP indeed functions to remove LRP from plasma.

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Example 3

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45 Experiments on the development of recombinant fVIII molecule with extended lifetime in circulation. Since recombinant fVIII products are widely used for fVIII replacement therapy in hemophiliacs who have decreased or nonfunctional fVIII, generation of mutant(s) with a prolonged lifetime is a promising approach to increase the efficacy and reduce the cost of fVIII infusion therapy. A 39 kDa receptor associated protein (RAP) binds reversibly to LRP and inhibits the binding of other ligands and therefore serves as a useful tool for

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10 testing whether LRP is involved in endocytosis of a given ligand. We found that
fVIII binding to LRP is inhibited by RAP, confirming the specificity of this
interaction. Since von Willebrand factor (vWF), bound to fVIII in the circulation,
does not inhibit fVIII binding to purified LRP, we proposed that removal of the
15 fVIII/vWF complex from the circulation may also be LRP-mediated. This role of
LRP was supported by our finding that the lifetime of human ¹²⁵I-fVIII/vWF
complex in mice was 2.5-times prolonged in the presence of RAP.

20 Based on our finding that fVIII amino acids 484-509 were important for
fVIII binding to LRP, these amino acids are also important for LRP-mediated
25 endocytosis. To identify the key fVIII amino acids required for endocytosis,
single residues 484-509 are mutated to Ala in the B- domain deleted fVIII (B(-)
fVIII). Since the basic residues are commonly involved in ligand binding to LRP,
six basic residues within 484-509 (3 Lys and 3 Arg) are mutated. U.S. Patent No.
30 55,859,204 discloses the substitution to Ala of three of these residues (Arg⁴⁸⁴,
Lys⁴⁹³ and Arg⁴⁹⁰); however the other 3 residues – Arg⁴⁹⁰, Lys⁴⁹⁶ and Lys⁴⁹⁹ – were
not substituted. Thus, these residues, individually and in combination, are
35 mutated to Ala. In particular, each of three Arg and each of three Lys are mutated
by pairs (this implies preparation of 9 additional fVIII Ala double-mutants).

40 It is then determined whether endocytosis of the vWF complexes with B(-)
45 fVIII mutant(s) by LRP-expressing cells is reduced compared to that of wild-type
B (-) fVIII/vWF. Some mutations result in a decreased rate of internalization and
a longer *in vivo* half-life of the complex of the B- fVIII mutant with vWF in
plasma of mice compared to that of wild type B- fVIII/vWF complex. The data
of the *in vivo* experiments performed in normal and fVIII-deficient mice is
mathematically analyzed using biphasic time-course clearance model and
equations approximating interspecies scaling which allow to predict fVIII half-life
in humans (*Toxicology and Applied Pharmacology* 136:75-78 (1996)).

50 Clearance of mutant fVIII in vWF-deficient mice which lack fVIII in
circulation (a mouse model for severe von Willebrand disease is described in
Proc. Natl. Acad. Sci. USA 95:9524-9529 (1998)) is also analyzed. These

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experiments are aimed at determining mutant fVIII's prolonged half-life in the absence of vWF. Factor VIII interaction with endothelial cells is also analyzed, since this interaction leads to fVIII internalization. In experiments using fluorescent microscopy techniques we observed uptake of fVIII by endothelial cells. Since a fine equilibrium exists in circulation between fVIII bound to vWF and fVIII bound and internalized by endothelial cells, fVIII interaction with phospholipid endothelial cell membrane is an important factor influencing concentration of fVIII (and hence its half-life) in circulation following fVIII injection.

Therefore, individual amino acids within the previously localized fVIII phospholipid binding site (C2 domain region 2303-2332) which play a role in fVIII binding to vWF and to phospholipid are identified. We identify the amino acids playing a key role in fVIII binding to phospholipid, but not to vWF. The amino acids which participate in fVIII binding to vWF and to phospholipids are selected based on the following observations. The homology search between the C2 domain of fVIII and the corresponding region of the discoidin and a family of homologous proteins, containing the so called DS domain, has revealed the fVIII C2 domain sequences involved in the formation of β -structures. In addition, it has been shown that the synthetic fVIII peptide 2310-2320 in which residues 2310 and 2320 are covalently linked to reproduce the corresponding loop structure within the C2 domain, competes for fVIII binding with vWF or phospholipid. Therefore, residues within the 2311-2319 region are mutated to Ala, and other amino acids. Since fV, a fVIII homolog, does not bind to vWF, we mutate only five residues which are unique within the 2311-2319 region of fVIII. The mutants are tested for binding to vWF and phospholipid, which identifies the fVIII residues playing a key role in binding to these ligands.

Clearance of the fVIII mutants with reduced phospholipid binding was compared with that of wt-fVIII in normal and hemophilic mice to determine the contribution of the phospholipid-dependent fVIII clearance component to total fVIII clearance.

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The mutations within the C2 domain region 2310-2320 prove to be effective for extension of fVIII lifetime in circulation, so we generate mutant fVIII in which both the C2 domain mutation(s) (positions 2310-2320) and mutation(s) within the A2 (positions 484-509) are combined.

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5 We test the designed extended lifetime fVIII for gene therapy purposes. The extended lifetime fVIII gene is inserted in a virus-based vector, and delivered into hemophilia A mice. The time course of the fVIII *in vivo* expression level is assessed as follows: the number of the gene copies per cell (hepatic), the gene transcription level, fVIII activity and the antigen level are determined. Since it was shown that high titer antibodies increase clearance of fVIII (*Br. J. Hematol.* 93:688-693 (1996)), we examine the immune response against the extended lifetime fVIII. We also compare its half-life in circulation in hemophilia A mice which formed antibodies against wild type fVIII.

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Claims

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What Is Claimed Is:

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1. A mutant factor VIII comprising an amino acid substitution at two or more positions in the A2 domain; wherein at least one of said amino acid substitutions is not at any of positions 484, 485, 487, 488, 489, 492, 493, 495, 501 or 508; wherein the mutant factor VIII has reduced receptor-dependent clearance; and wherein the mutant factor VIII has procoagulant activity.

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2. The mutant factor VIII of claim 1, which lacks the B domain.

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3. The mutant factor VIII of claim 2, comprising an amino acid substitution at two or more of positions 484 to 509.

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4. The mutant factor VIII of claim 3, comprising an amino acid substitution at two or more of positions 490, 496 or 499.

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5. The mutant factor VIII of claim 3, comprising an amino acid substitution at one or more of positions 490, 496 or 499; and at one or more of positions 484, 489 or 493.

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6. The mutant factor VIII of claim 5, comprising an amino acid substitution at position 490; and at one or more of positions 484, 489 or 493.

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7. The mutant factor VIII of claim 5, comprising an amino acid substitution at position 496; and at one or more of positions 484, 489 or 493.

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8. The mutant factor VIII of claim 5, comprising an amino acid substitution at position 499; and at one or more of positions 484, 489 or 493.

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9. The mutant factor VIII of claim 2, comprising SEQ ID NO:5.

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10. A pharmaceutically acceptable composition comprising the mutant factor VIII of claim 2.

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11. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the mutant factor VIII of claim

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12. The method of claim 11, which further comprises administering an effective amount of receptor associated protein (RAP).

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13. A polynucleotide encoding the mutant factor VIII of claim 2.

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14. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the polynucleotide of claim 13.

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15. The method of claim 14, which further comprises administering an effective amount of a polynucleotide encoding RAP.

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16. A mutant factor VIII comprising an amino acid substitution at one or more positions in the A2 domain, which is not at any of positions 484, 485, 487, 488, 489, 492, 493, 495, 501 or 508; wherein the mutant factor VIII has reduced receptor-dependent clearance; and wherein the mutant factor VIII has procoagulant activity.

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17. The mutant factor VIII of claim 16, which lacks the B domain.

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18. The mutant factor VIII of claim 17, comprising an amino acid substitution at one or more of positions 484 to 509.

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19. The mutant factor VIII of claim 18, comprising an amino acid substitution at one or more of positions 490, 496 or 499.

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20. The mutant factor VIII of claim 19, comprising an amino acid substitution at position 490.

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5 21. The mutant factor VIII of claim 19, comprising an amino acid substitution at position 496.

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22. The mutant factor VIII of claim 19, comprising an amino acid substitution at position 499.

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23. The mutant factor VIII of claim 17, comprising SEQ ID NO:5.

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24. A pharmaceutically acceptable composition comprising the mutant factor VIII of claim 17.

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35 25. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the mutant factor VIII of claim 17.

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26. The method of claim 25, which further comprises administering an effective amount of RAP.

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27. A polynucleotide encoding the mutant factor VIII of claim 17.

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28. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the polynucleotide of claim 27.

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29. The method of claim 28, which further comprises administering
an effective amount of a polynucleotide encoding RAP.

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30. A mutant factor VIII comprising an amino acid substitution at one
or more positions in the C2 domain; wherein the mutant factor VIII has reduced
15 5 receptor-independent clearance; and wherein the mutant factor VIII has
procoagulant activity.

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31. The mutant factor VIII of claim 30, which lacks the B domain.

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32. The mutant factor VIII of claim 31, comprising an amino acid
substitution at one or more of positions 2303 to 2332.

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10 33. The mutant factor VIII of claim 32, comprising an amino acid
substitution at one or more of positions 2311 to 2319.

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34. The mutant factor VIII of claim 31, comprising SEQ ID NO:1.

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35. A pharmaceutically acceptable composition comprising the mutant
factor VIII of claim 31.

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15 36. A method of treating hemophilia which comprises administering
to a patient in need thereof an effective amount of the mutant factor VIII of claim
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37. The method of claim 36, which further comprises administering
an effective amount of RAP.

20 38. A polynucleotide encoding the mutant factor VIII of claim 31.

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39. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the polynucleotide of claim 38.

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40. The method of claim 39, which further comprises administering an effective amount of a polynucleotide encoding RAP.

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5 41. A mutant factor VIII comprising:

20 (i) an amino acid substitution at two or more positions in the A2 domain; wherein at least one of said amino acid substitutions is not at any of positions 484, 485, 487, 488, 489, 492, 493, 495, 501 or 508; and

10 (ii) an amino acid substitution at one or more positions in the C2 domain as numbered in SEQ ID NO:1;

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wherein the mutant factor VIII has reduced clearance; and wherein the mutant factor VIII has procoagulant activity.

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30 42. The mutant factor VIII of claim 41, which lacks the B domain.

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43. The mutant factor VIII of claim 42, comprising SEQ ID NO:5.

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15 44. A pharmaceutically acceptable composition comprising the mutant factor VIII of claim 42.

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45. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the mutant factor VIII of claim 42.

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20 46. The method of claim 45, which further comprises administering an effective amount of RAP.

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47. A polynucleotide encoding the mutant factor VIII of claim 42.

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57. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the polynucleotide of claim 56.

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58. The method of claim 57, which further comprises administering an effective amount of a polynucleotide encoding RAP.

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59. A polypeptide selected from the group consisting of:

(a) a polypeptide comprising a fragment of receptor-associated protein (RAP) which binds LRP;

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(b) a polypeptide comprising a mutant of RAP which binds LRP;

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(c) a polypeptide comprising an analog of RAP which binds LRP;

(d) a polypeptide comprising 20 contiguous amino acids of the sequence of SEQ ID NO:4, which binds LRP; and

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(e) a polypeptide comprising amino acids 203 to 319 of SEQ

15 ID NO:4.

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60. A pharmaceutically acceptable composition comprising the polypeptide of claim 59.

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61. A method of treating hemophilia which comprises administering to a patient in need thereof an effective amount of the polypeptide of claim 59.

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20 62. The method of claim 61, which further comprises administering a mutant factor VIII having an amino acid substitution at one or more positions in the A2 domain.

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63. The method of claim 61, which further comprises administering a mutant factor VIII having an amino acid substitution at one or more positions in the C2 domain.

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64. The method of claim 61, which further comprises administering a mutant factor VIII having an amino acid substitution at one or more positions in the A2 domain and an amino acid substitution at one or more positions in the C2 domain.

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65. A method of increasing the half-life of factor VIII, selected from the group consisting of:

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(a) a method which comprises substituting an amino acid at two or more positions in the A2 domain; wherein at least one of said amino acid substitutions is not at any of positions 484, 485, 487, 488, 489, 492, 493, 495, 501 or 508; wherein the resulting factor VIII has reduced receptor-dependent clearance; and wherein the resulting factor VIII has procoagulant activity;

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(b) method which comprises substituting an amino acid at one or more positions in the A2 domain, which is not at any of positions 484, 485, 487, 488, 489, 492, 493, 495, 501 or 508; wherein the resulting factor VIII has reduced receptor-dependent clearance; and wherein the resulting factor VIII has procoagulant activity;

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(c) a method which comprises substituting an amino acid at one or more positions in the C2 domain; wherein the resulting factor VIII has reduced receptor-independent clearance; and wherein the resulting factor VIII has procoagulant activity;

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(d) a method which comprises administering to a patient in need thereof an effective amount of a fragment of RAP, wherein said fragment binds LRP; and

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(e) a method comprising two or more of methods (a), (b), (c) or (d).

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FIG. 1

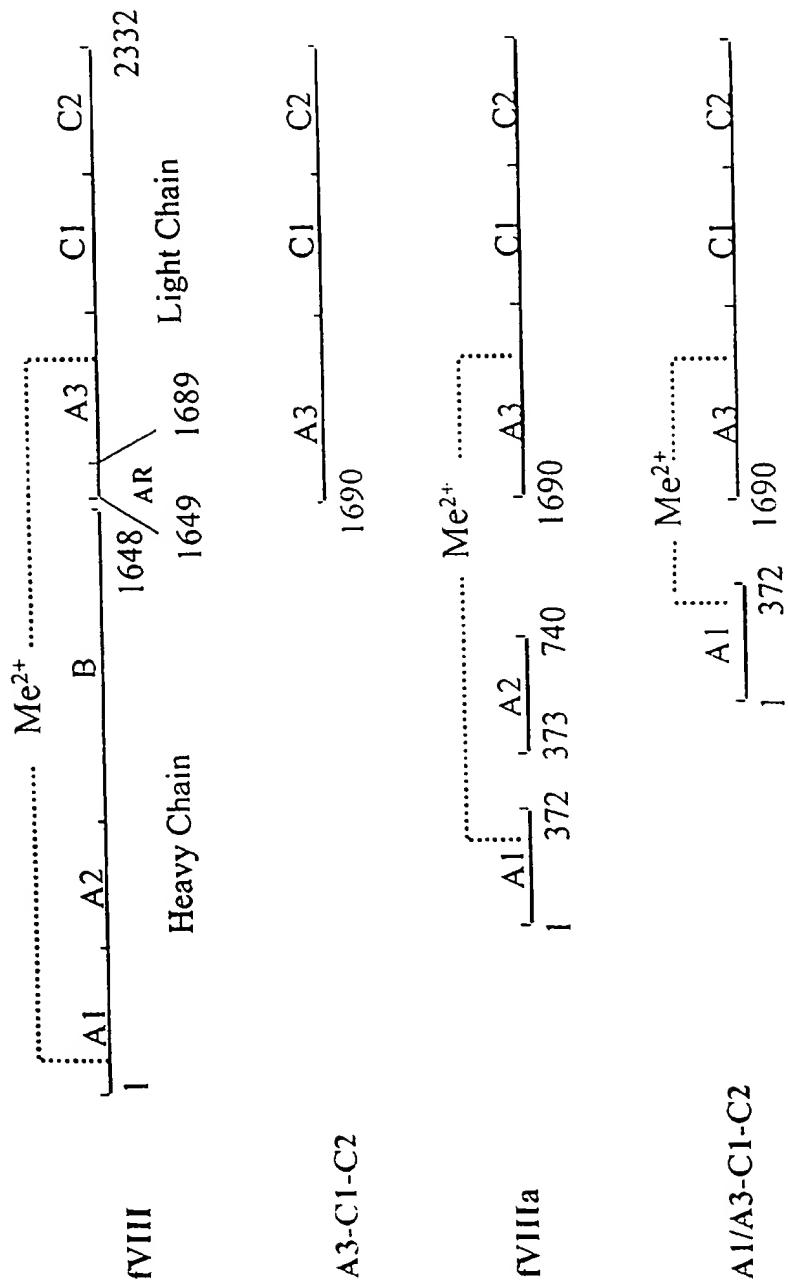


FIG. 2A

ATRRYYLGAVELSWDYMQSDLGELP
VDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHFLNIAKPRPPWMGLLGPLTIQAEVYDT
VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSH
QHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNPSFIQIRS
VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSOYLNNGPQIGRKYKKVRFMAY
TDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNOASRPYNIYPHGITDVRPLYSR
A2_Domain *****
LRP
RLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYSSFVNMERDLASGL

Binding Region
IGPLLICYKESVDORGNOIMSDKRNVILFSVFDENRSWYLTENIORFLPNPAGVOLED
PEFOASNIMHSINGYVFDSLLOSVCLHEVAYWYIISIGAOTDFLSVFFSGYTFKHKMV
YEDTLTLPFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYED
SYEDISAYLLSKNNAIEPREITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQS
PRSFQKKTRHYF1AAVERI.WDYGMSSSPHVLRNRAQSGSVPQFKVVFQEFTDGSFTQ

FIG. 2B

PLYRGELNEHLGLLGPYIRAEVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEP
KNFVKPNETKTYFWKVQHHMAPTKDEFDCAWAYFSDVDLEKDVHSGLIGPLLVCNT
TLNPAHGRQVTVQEFAFFTFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFH
AINGYIMDTLPGLVMAQDQRIRWYLLSMGSNEIHSIHFSGHVFTVRKKEEYKALYN
LYPGVFETVEMPLSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDF
QITASGQYQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKF
SSLYISQFIIMYSLDGKKWQTYRGNSTGTLVFFGNVDSSGIKHNIFNPPIIARYIRL
HPTHYSIRSTLRLMELMGCDLNCSMPLGMESKAISDAQITASSYFTNMFTWSPSKAR
LHLQGRSNAWRPQVNNPKEWLQVDFQKTMKVGVTTQGVKSLLTSMYVKEFLISSQD
GHQWTLFFQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLG
CEAQDLY

FIG. 3A

1 MQIELSTCF ECLLRECFS ATRYYLGA VE LSWDYMQS DL GELPV DARFP PRV PKSF PPN
61 TSVVYKKT LVE FETDHLF NI AKPRPPWM G I. LGPTIQA E VY DTVVITLKNM ASHPVSLH AV
121 GVS YWKASEG A EYDDOTSQR EKEODKVF PG GSHTYVWQVL KENGPMASDP LCLTYSYLSH
181 VDLVKDLNSG LIGALLVCRE GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
241 AASARAWPKM HTVNGYVNRS LPGLIGCHR K SYW HVIGMG TTPEVHSI FL EGHTFLVRNH
301 RQASLEISPI TFLTAQTLLM DLGQFLLFC H ISSHQHDGM E AYVKVDSCPE EPOLRMKNNE
361 EAEDYDDDLT DSEM DVVRFD DDNSPSFIQI RSVAKKHPKT W VYIA A EEE DWDYAPLVLA
421 PDDRSYKSQY LNNGPQRIGR KYKKVRFMAY TDETFK TREA IQHESGILGP LLYGEVGOTL
481 LIIFKNOASR PYNIYPHG IT D VRPLYSRRL PKGVKHLKDF PILPGEIF KY KWTVTVEDGP
541 TKSDPRCLTR YYSSFVNMR DLSAGLIGPL L I C Y K E S V D Q RGNQIMSDKR NVILFSV FDE
601 NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGV FDSLQLSVCL HEVAYWYI LS
661 IGAQTDFLSV FFSGYTFKIK MVYEDT LTLF PFSGETVFMS MENPGLWI LG CHNSDFRN R G
721 MTALLKVSSC DKNTGDYYED SYEDISAYL SKNNAI EPRS FSQNSRHRST RQKQFNATTI
781 PENDIEKTDP WFAHRT PMPK IQNVSSSDIL MLLRQSPTPH GLSLSDIQEA KYETFSDDPS
841 PGAI DSNNSL SEMTHFRPQL HHSGDMVFTF ESGLQLRLNE KLTAA TEL KKLD FKVS ST
901 SNNLISTIPS DNLAAGTDNT SSLGPPSMPV HYD S O L D T T L F G K K S S P L T E S G G P L S I S E E
961 NND SKLLESG LMNSQESSWG K N V S S T E S G R L F K G K R A H G P A L L T K D N A L F K V S I S L L K T N
1021 KTSNNSATNR KTHIDG P S L L I F N S P S V W Q N I E S D T E F K K T P L I H D R M L M D K N A T A L R L
1081 NHMSNKT TSS K NMEMVQQKK E G P I P P D A Q N P D M S F F K M L F L P E S A R W I Q R T H G K N S L N S G
1141 QGPSPKQLVS LGPEKSVEGQ N F L S E K N K V V V G K G E F T K D V G L K E M V F P S S R N L F L T N L D N
1201 L H E N N T H N Q E K K I Q E E I E K K E T L I Q E N V V L P Q I H T V T G T K N F M K N L F L L S T R Q N V E G S Y D
1261 GAYAPV LQDF RSLNDSTNR T K K H T A H F S K K G E F E N L E G L G N Q T K Q I V E K Y A C T T R I S P N T
1321 SQQN FVT QRS K R A L K Q F R L P L E E T E L E K R I I V D D T S T Q W S K N M K H L T P S T L T Q I D Y N E K E
1381 KGAITQSPLS DCLTRSHSIP QANRSPLPIA KVSSFPSTIRP IYLTRVLFQD NSSHLP AASY
1441 RKKDSGVQES SH E L Q G A K K N N L S L A I L T L E M T G D Q R E V G S L G T S A T N S V T Y K K V E N T V I P
1501 K P D L P K T S G K V E I L P K V H I Y Q K D L F P T E T S N G S P G H L D I V E G S L L Q G S T E G A I K W N E A N R P
1561 G K V P F L R V A T E S S A K T P S K L L D P I A W D N H Y G T O I P K E E W K S Q E K S P E K T A F K K K D T I L S L
1621 N A C E S N H A I A A I N E G Q N K P E I E V T W A K Q G R T F R I C S Q N P P V L K R H Q R E I T R T T L Q S D Q E E

FIG. 3B

1681 IDYDUTISVE MKKEDFDIYD EDENQSPRSF QKKTRHYFIA AVERLWDYGM SSSPHVLRNR
1741 AQSGSVPQPK KVVFQEFTDG SFTQPLYRGE LNEHLGLGP YIRAEVEDNI MVTFRNQASR
1801 PYSFYSSLIS YEEQRQGAE PRKNFVKPNE TKTYFWKVQH HMAPTKDEFD CKAWAYFSDV
1861 DLEKDVHSGL IGPLLVCNTN TLNPAHGRQV TVQEFALEFTT IFDETKSWYF TENMERNCRA
1921 PCNIQMEDPT FKENYRFHAI NGYIMDTLPG LVMAQDQRIR WYLLSMGSNE NIHSIHESGH
1981 VFTVRKKEEY KMALYNLYPG VFETVEMI.PS KAGIWRVECL IGEILHAGMS TLFLVYSNKC
2041 QTPLGMASGH IRDFQITASG QYGCWAPKLA RLHYSGSINA WSTKEPFSWI KVDLLAPMII
2101 HGIKTQGARQ KFSSLYISQF IIMYSLDGKK WQTYRGNSTG TLMVFFGNVD SSGIKHNEN
2161 PPIIAKYIRL HPTHYSIRST LRMELMGCDL NSCSMPLGME SKAISDAQIT ASSYFTNMFA
2221 TWSPSKARLH LQGRSNAWRP QVNNPKEWLQ VDFQKTMKVT GVTTQGVKSL LTSMYVKEFL
2281 ISSSQDGHQW TLFFQNGKVK VFQGNQDSFT PVVNSLDPL LTRYLRIHPQ SWVHQIALRM
2341 EVLGCEAQDL *

FIG. 4

1 MAPRRVRSFL RGLPALLLLL LFLGPWPAAS HGGKYSREKN QPKPSPKRES GEEFRMEKLN
Signal Sequence

61 QLWEKAQRLH LPPVRLAELH ADLKIQERDE LAWKKLKLDG LDEGEKEAR LIRNLNVILA

121 KYGLDGKKDA RQVTSNSLSC TQEDGLDDPR LEKLWHKAKT SGKFSGEELD KLWREFLHHK

181 EKVHEYNVLL ETLSRTEEIH ENVISPSDLS DIKGSVLHSR HTELKEKLRS INQGLDRLRR

241 VSHQGYSTEA EFEEPRVIDL WDLAQSANLT DKELEAFREE LKHFEAKIEK HNHYQKQLEI

LDL Binding Region

301 AHEKLRHAES VGDGERVSRS REKHALLEGR TKELGYTUVKK HLQDLSGRIS RARHNL

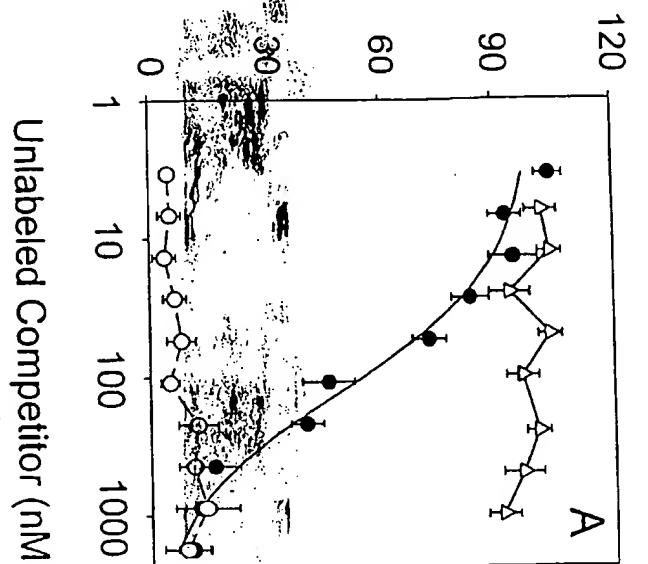
7 / 14
125I-fVIII Binding (% of Control)

FIG. 5

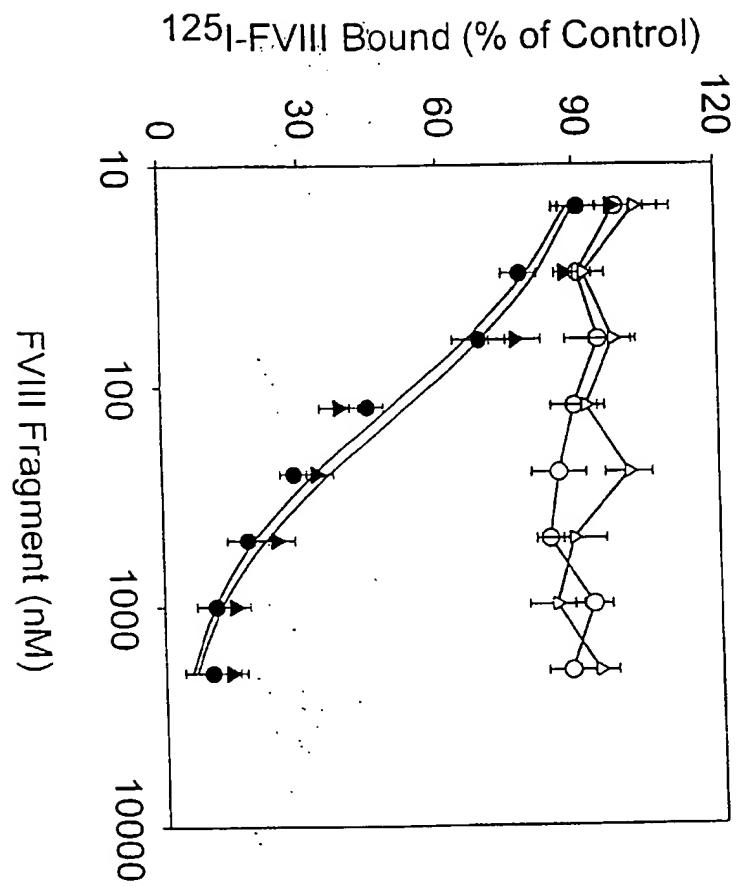


FIG. 6

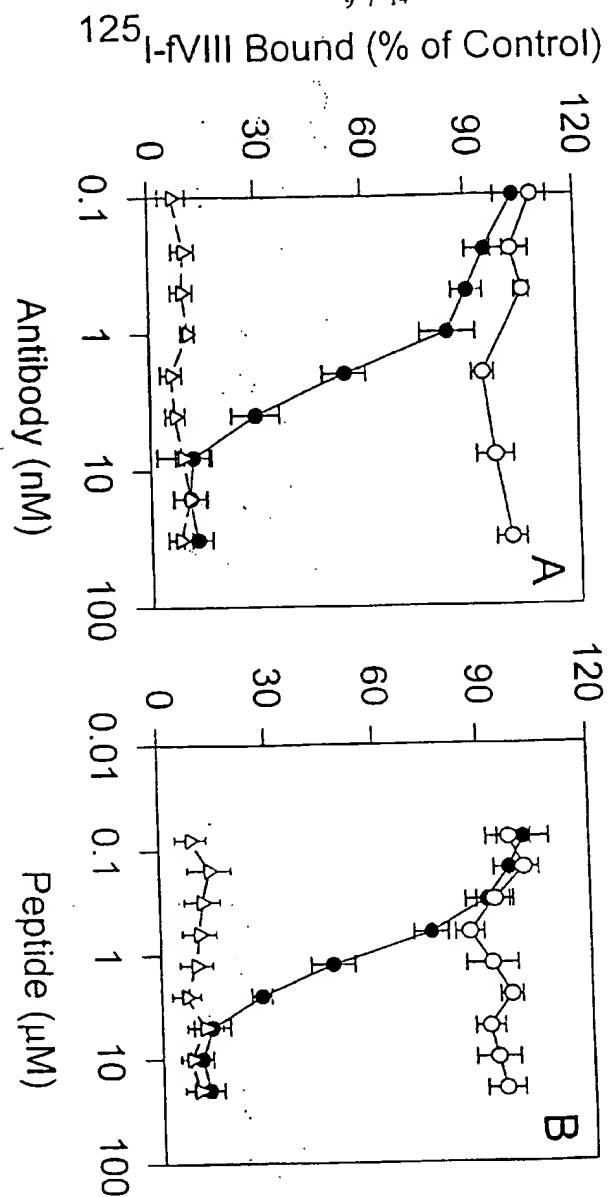


FIG. 7

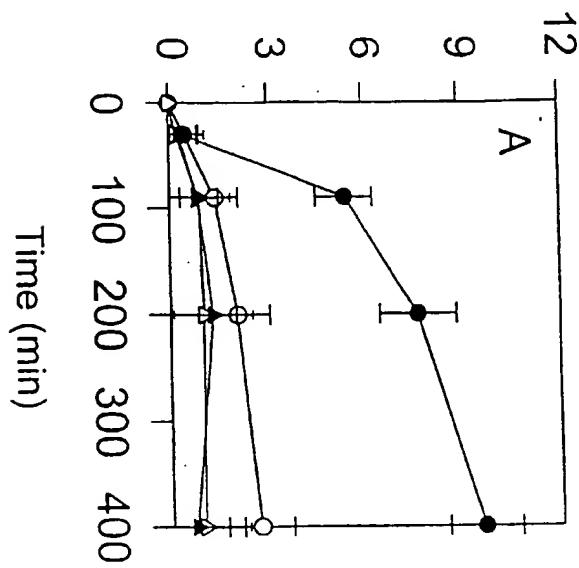
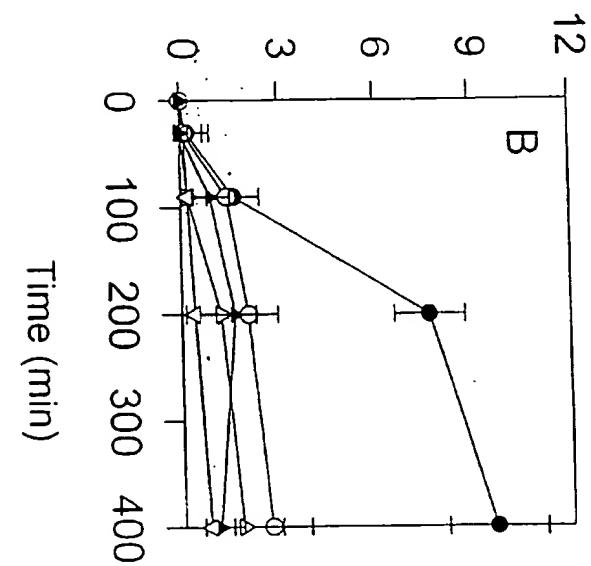
10 / 14
Fmoles Internalized/ 10^5 CellsFmoles Degraded/ 10^5 Cells

FIG. 8

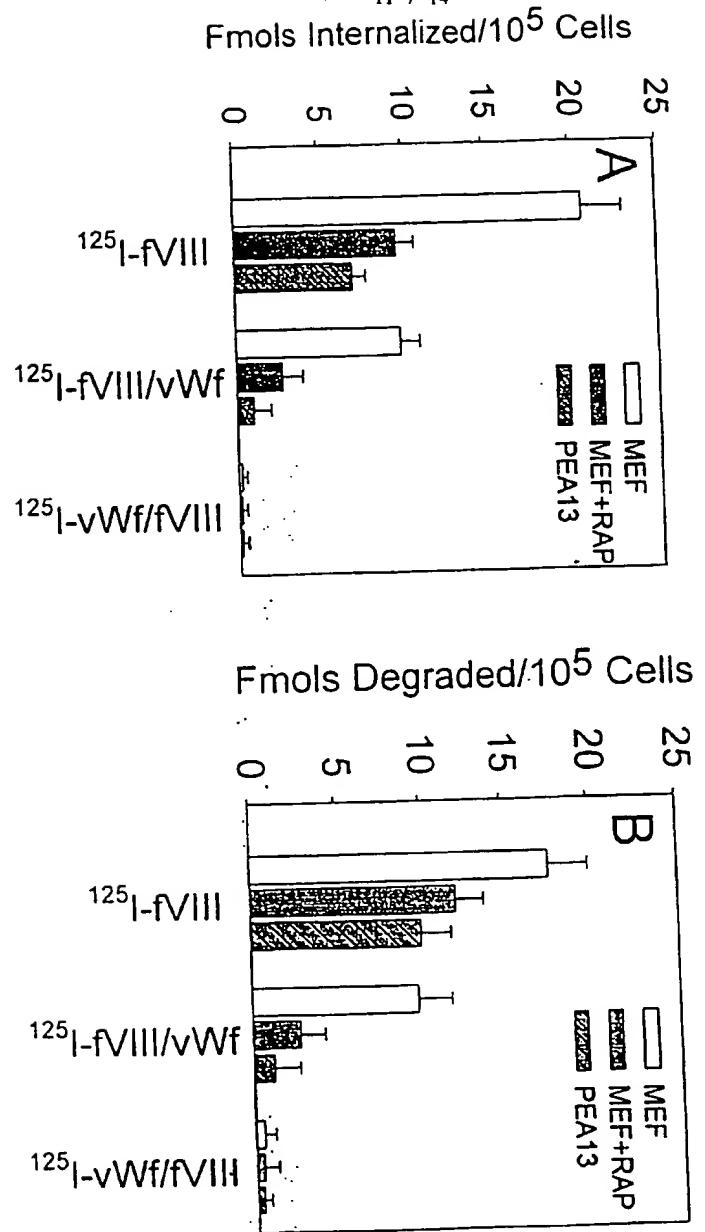


FIG. 9

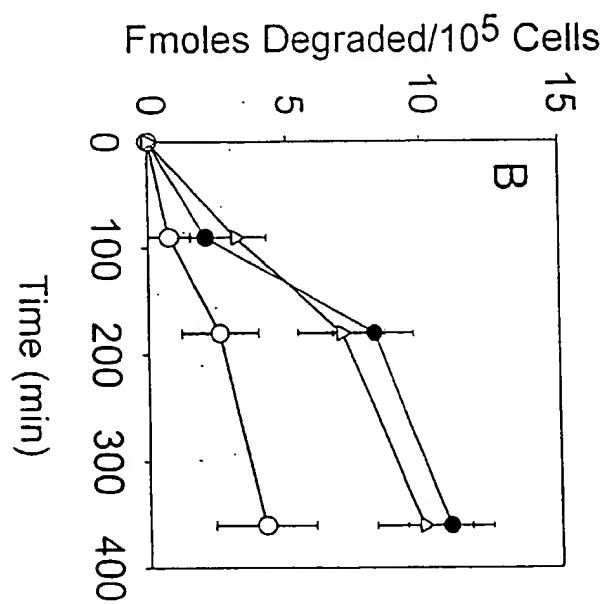
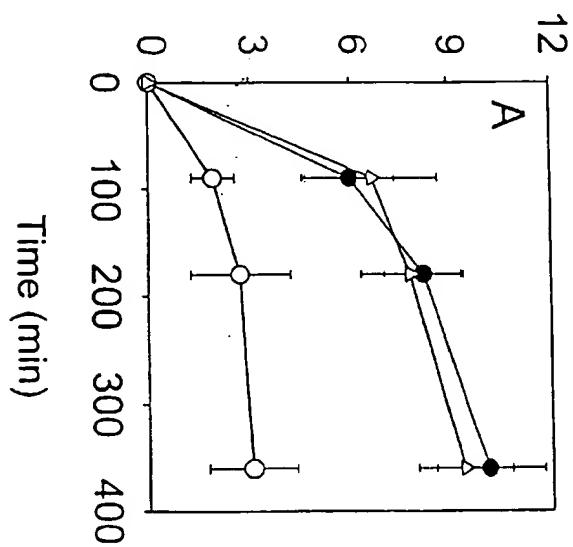
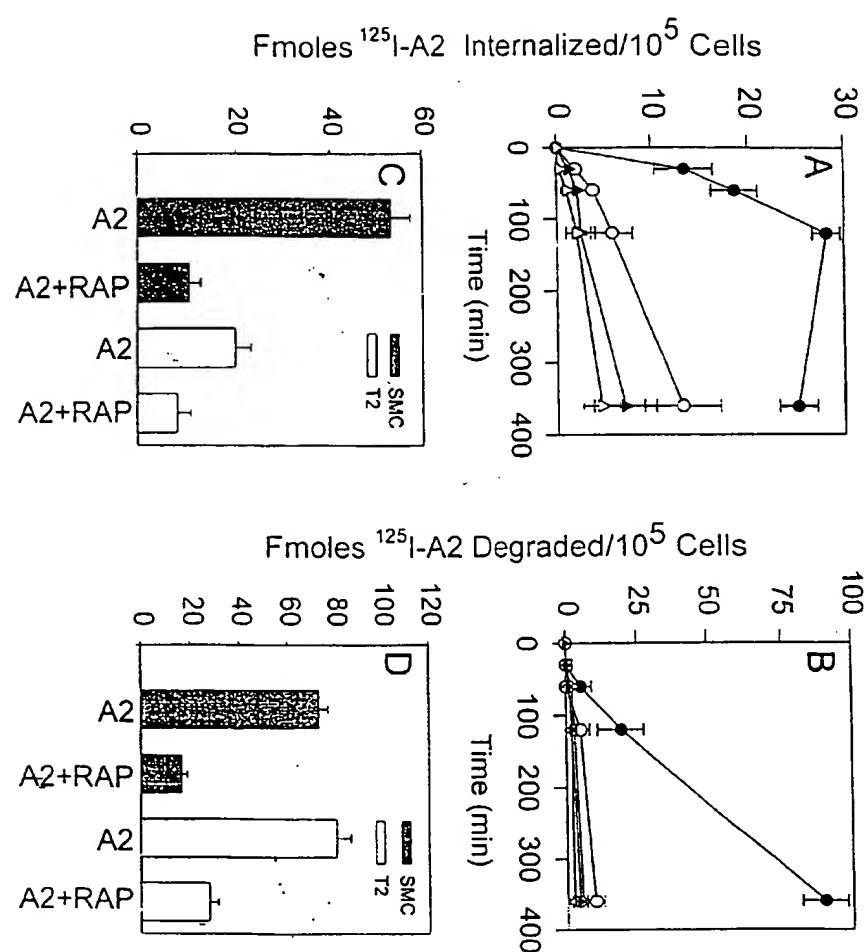
Fmoles Internalized/ 10^5 Cells

FIG. 10



125I-Radioactivity Remaining in Plasma (%)

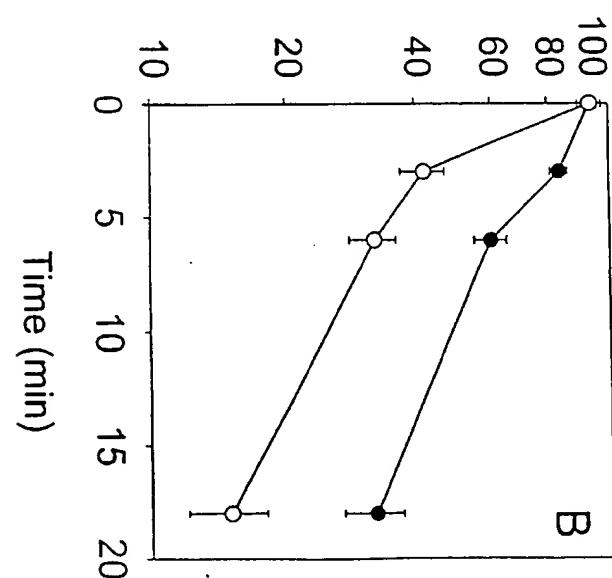
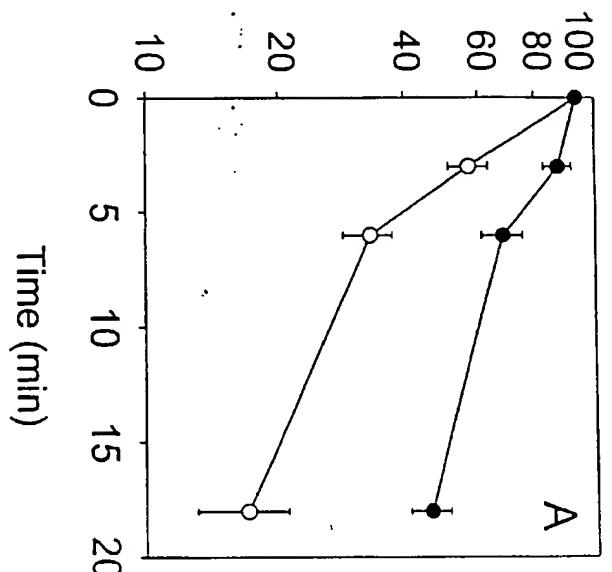


FIG. 12

-1-

SEQUENCE LISTING

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Saenko, Evgueni L.
Strickland, Dudley K.

<120> Methods of Reducing Factor VIII Clearance and
Compositions Therefor

<130> 1327.059PC01

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<151> 1999-05-24

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gaagaattaa ccttttgctt ctccagttga acatttgttag caataagtc atg caa ata 118
Met Gln Ile

-2-

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 Glu Leu Ser Thr Cys Phe Phe Leu Cys Ieu Leu Arg Phe Cys Phe Ser
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 gcc acc aga aga tac tac ctg ggt gca gtg gaa ctg tca tgg gac tat 214
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 Met Gin Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
 20 25 30

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 Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
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 Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
 50 55 60

 agg cca ccc tgg atg ggt ctg cta ggt cct acc atc cag gct gag gtt 406
 Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
 65 70 75 80

 tat gat aca gtg gtc att aca ctt aag aac atg gct tcc cat cct gtc 454
 Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
 85 90 95

 agt ctt cat gct gtt ggt gta tcc tac tgg aaa gct tct gag gga gct 502
 Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
 100 105 110

 gaa tat gat gat cag acc agt caa agg gag aaa gaa gat gat aaa gtc 550
 Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
 115 120 125

 ttc cct ggt gga agc cat aca tat gtc tgg cag gtc ctg aaa gag aat 598
 Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
 130 135 140

 ggt cca atg gcc tct gac cca ctg tgc ctt acc tac tca tat ctt tct 646
 Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
 145 150 155 160

 cat gtg gac ctg gta aaa gac ttg aat tca ggc ctc att gga gcc cta 694

-3-

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu			
165	170	175	
cta gta tgt aga gaa ggg agt ctg gcc aag gaa aag aca cag acc ttg	742		
Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu			
180	185	190	
cac aaa ttt ata cta ctt ttt gct gta ttt gat gaa ggg aaa agt tgg	790		
His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp			
195	200	205	
cac tca gaa aca aag aac tcc ttg atg cag gat agg gat gct gca tct	838		
His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser			
210	215	220	
gct cgg gcc tgg cct aaa atg cac aca gtc aat ggt tat gta aac agg	886		
Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg			
225	230	235	240
tct ctg cca ggt ctg att gga tgc cac agg aaa tca gtc tat tgg cat	934		
Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His			
245	250	255	
gtg att gga atg ggc acc act cct gaa gtg cac tca ata ttc ctc gaa	982		
Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu			
260	265	270	
ggt cac aca ttt ctt gtg agg aac cat cgc cag gcg tcc ttg gaa atc	1030		
Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile			
275	280	285	
tcg cca ata act ttc ctt act gct caa aca ctc ttg atg gac ctt gga	1078		
Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly			
290	295	300	
cag ttt cta ctg ttt tgt cat atc tct tcc cac caa cat gat ggc atg	1126		
Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met			
305	310	315	320
gaa gct tat gtc aaa gta gac agc tgt cca gag gaa ccc caa cta cga	1174		
Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg			
325	330	335	
atg aaa aat aat gaa gaa gcg gaa gac tat gat gat gat ctt act gat	1222		
Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp			

-4-

340 345 350

tct gaa atg gat gtg gtc agg ttt gat gat gac aac tct cct tcc ttt 1270
 Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
 355 360 365

atc caa att cgc tca gtt gcc aag aag cat cct aaa act tgg gta cat 1318
 Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
 370 375 380

tac att gct gct gaa gag gag gac tgg gac tat gct ccc tta gtc ctc 1366
 Tyr Ile Ala Ala Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
 385 390 395 400

gcc ccc gat gac aqa agt tat aaa agt caa tat ttg aac aat ggc cct 1414
 Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
 405 410 415

cag cgg att ggt agg aag tac aaa aaa gtc cga ttt atg gca tac aca 1462
 Gln Arg Ile Gly Arg Lys Tyr Lys Val Arg Phe Met Ala Tyr Thr
 420 425 430

gat gaa acc ttt aag act cgt gaa gct att cag cat gaa tca gga atc 1510
 Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
 435 440 445

ttg gga cct tta ctt tat ggg gaa gtt gga gac aca ctg ttg att ata 1558
 Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
 450 455 460

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 Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
 465 470 475 480

act gat gtc cgt cct ttg tat tca agg aga tta cca aaa ggt gta aaaa 1654
 Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
 485 490 495

cat ttg aag gat ttt cca att ctg cca gga gaa ata ttc aaa tat aaaa 1702
 His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
 500 505 510

tgg aca gtg act gta gaa gat ggg cca act aaa tca gat cct cgg tgc 1750
 Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
 515 520 525

-5-

ctg acc cgc tat tac tct agt ttc gtt aat atg gag aga gat cta gct	1798
Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala	
530 535 540	
tca gga ctc att ggc cct ctc atc tgc tac aaa gaa tct gta gat	1846
Ser Gly Ieu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp	
545 550 555 560	
caa aga gga aac cag ata atg tca gac aag agg aat gtc atc ctg ttt	1894
Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe	
565 570 575	
tct gta ttt gat gag aac cga agc tgg tac ctc aca gag aat ata caa	1942
Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln	
580 585 590	
cgc ttt ctc ccc aat cca gct gga gtg cag ctt gag gat cca gag ttc	1990
Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe	
595 600 605	
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Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser	
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625 630 635 640	
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Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr	
645 650 655	
acc ttc aaa cac aaa atg gtc tat gaa gac aca ctc acc cta ttc cca	2182
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Phe Pro	
660 665 670	
ttc tca gga gaa act gtc ttc atg tcc atg gaa aac cca ggt cta tgg	2230
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp	
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att ctg ggg tgc cac aac tca gac ttt cgg aac aga ggc atg acc gcc	2276
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala	
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-6-

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gac	agt	tat	gaa	gat	att	tca	gca	tac	ttg	ctg	agt	aaa	aac	aat	gcc	2374
Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala	
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Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Ser	Arg	His	Arg	Ser	Thr	Arg		
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Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys	
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Thr	Asp	Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn	
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Val	Ser	Ser	Asp	Leu	'Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro		
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cat	ggg	cta	tcc	tta	tct	gat	ctc	caa	gaa	gcc	aaa	tat	gag	act	ttt	2614
His	Gly	Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe	
				805					810				815			
tct	gat	gat	cca	tca	cct	gga	gca	ata	gac	agt	aat	aac	agc	ctg	tct	2662
Ser	Asp	Asp	Pro	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Ile	Ser		
				820					825				830			
gaa	atg	aca	cac	tcc	agg	cca	cag	ctc	cat	cac	agt	ggg	gac	atg	gta	2710
Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val	
				835					840				845			
ttt	acc	cct	gag	tca	ggc	ctc	caa	tta	aga	tta	aat	gag	aaa	ctg	ggg	2758
Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly	
				850					855				860			
aca	act	gca	gca	aca	gag	ttg	aag	aaa	ctt	gat	ttc	aaa	gtt	tct	agt	2806
Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser	
				865					870				875			880
aca	tca	aat	aat	ctg	att	tca	aca	att	cca	tca	gac	aat	ttg	gca	gca	2854

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Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala			
885	890	895	
gg t ct gat aat aca agt tcc tta gga ccc cca agt atg cca gtt cat 2992			
Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His			
900	905	910	
tat qat agt caa tta gat acc act cta ttt ggc aaa aag tca tct ccc 2950			
Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro			
915	920	925	
ctt act gag tct ggt gga cct ctg agc ttg agt gaa gaa aat aat gat 2998			
Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp			
930	935	940	
tca aag ttg tta gaa tca ggt tta atg aat agc caa gaa agt tca tgg 3046			
Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp			
945	950	955	960
gca aaa aat gta tcg tca aca gag agt ggt agg tta ttt aaa ggg aaa 3094			
Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys			
965	970	975	
aga gct cat gga cct gct ttg ttg act aaa gat aat gcc tta ttc aaa 3142			
Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys			
980	985	990	
gtt agc atc tct ttg tta aag aca aac aaa act tcc aat aat tca gca 3190			
Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala			
995	1000	1005	
act aat aga aag act cac att gat ggc cca tca tta tta att gag aat 3238			
Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu Ile Glu Asn			
1010	1015	1020	
agt cca tca gtc tgg caa aat ata tta gaa agt gac act gag ttt aaa 3286			
Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu Phe Lys			
1025	1030	1035	1040
aaa gtg aca cct ttg att cat gac aga atg ctt atg gac aaa aat gct 3334			
Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp Lys Asn Ala			
1045	1050	1055	
aca gct ttg agg cta aat cat atg tca aat aaa act act tca tca aaa 3382			
Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser Lys			

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1060 1065 1070

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 Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp
 1075 1080 1085

gca cca aat cca gat atg tcg ttc ttt aag atg cta ttc ttg cca gaa 3478
 Ala Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu
 1090 1095 1100

tca gca acg tgg ata caa agg act cat gga aag aac tct ctg aac tct 3526
 Ser Ala Arg Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser
 1105 1110 1115 1120

ggc caa ggc ccc agt cca aag caa tta gta tcc tta gga cca gaa aaa 3574
 Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys
 1125 1130 1135

tct gtc gaa ggt cag aat ttc ttg tct gag aaa aac aaa gtc gta gta 3622
 Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val
 1140 1145 1150

gca aag ggt gaa ttt aca aag gac gta gga ctc aaa gag atg gtt ttt 3670
 Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe
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cca agc agc aga aac cta ttt ctt act aac ttg gat aat tta cat gaa 3718
 Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
 1170 1175 1180

aat aat aca cac aat caa gaa aaa aaa att cag gaa gaa ata gaa aag 3766
 Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu Lys
 1185 1190 1195 1200

aac gaa aca tta atc caa gag aat gta gtt ttg cct cag ata cat aca 3814
 Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
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gtg act ggc act aag aat ttc atg aag aac ctt ttc tta ctg agc act 3862
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Ser Thr
 1220 1225 1230

agg caa aat gta gaa ggt tca tat gac ggg gca tat gct cca gta ctt 3910
 Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu
 1235 1240 1245

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caa gat ttt agg tca tta aat gat tca aca aat aga aca aag aaa cac 3958
 Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His
 1250 1255 1260

aca gct cat ttc tca aaa aaa ggg gag gaa gaa aac ttg gaa ggc ttg 4006
 Thr Ala His Phe Ser Lys Lys Gly Glu Glu Asn Leu Glu Gly Leu
 1265 1270 1275 1280

gga aat caa acc aag caa att gta gag aaa tat gca tgc acc aca agg 4054
 Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys Thr Thr Arg
 1285 1290 1295

ata tct cct aat aca agc cag cag aat ttt gtc acg caa cgt agt aag 4102
 Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln Arg Ser Lys
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aga gct ttg aaa caa ttc aga ctc cca cta gaa gaa aca gaa ctt gaa 4150
 Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr Glu Leu Glu
 1315 1320 1325

aca agg ata att gtg gat gac acc tca acc cag tgg tcc aaa aac atg 4198
 Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn Met
 1330 1335 1340

aaa cat ttg acc ccg agc acc ctc aca cag ata gac tac aat gag aag 4246
 Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys
 1345 1350 1355 1360

gag aaa ggg gcc att act cag tct ccc tta tca gat tgc ctt acg agg 4294
 Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg
 1365 1370 1375

agt cat agc atc cct caa gca aat aga tct cca tta ccc att gca aag 4342
 Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys
 1380 1385 1390

gta tca tca ttt cca tct att aga cct ata tat ctg acc agg gtc cta 4390
 Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu
 1395 1400 1405

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 Phe Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys
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-10-

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 Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys Lys
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aat aac ctt tct tta gcc,att cta acc ttg gag atg act ggt gat caa 4534
 Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly Asp Gln
 1445 1450 1455

aga gag gtt ggc tcc ctg ggg aca agt gcc aca aat tca gtc aca tac 4582
 Arg Gln Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr Tyr
 1460 1465 1470

aag aaa gtt gag aac act gtt ctc ccg aaa cca gac ttg ccc aaa aca 4630
 Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr
 1475 1480 1485

tct ggc aaa gtt gaa ttg ctt cca aaa gtt cac att tat cag aag gac 4678
 Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp
 1490 1495 1500

cta ttc cct acg gaa act agc aat ggg tct cct ggc cat ctg gat ctc 4726
 Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu
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gtg gaa ggg agc ctt ctt cag gga aca gag gga gcg att aag tgg aat 4774
 Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn
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gaa gca aac aga cct gga aaa gtt ccc ttt ctg aga gta gca aca gaa 4822
 Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val Ala Thr Glu
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 Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu Ala Trp Asp
 1555 1560 1565

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 Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu
 1570 1575 1580

aag tca cca gaa aaa aca gct ttt aag aaa aag gat acc att ttg tcc 4966
 Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Asp Thr Ile Leu Ser
 1585 1590 1595 1600

ctg aac gct tgt gaa agc aat cat gca ata gca gca ata aat gag gga 5014

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Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
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 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr
 1620 1625 1630
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 gaa aac ctg tgc tct caa aac cca cca gtc ttg aaa cgc cat caa cgg 5110
 Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gin Arg
 1635 1640 1645
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 Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr
 1650 1655 1660
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 gat gat acc ata tca gtt gaa atg aag aag gaa gat ttt gac att tat 5206
 Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr
 1665 1670 1675 1680
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 gat gag gat gaa aat cag agc ccc cgc agc ttt caa aag aaa aca cga 5254
 Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg
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 His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser
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 Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro
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 Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg
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1780

1785

1790

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Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys			
1795	1800	1805	
cct aat gaa acc aaa act tac ttt tgg aaa gtg caa cat cat atg gca	5638		
Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala			
1810	1815	1820	
ccc act aaa gat gag ttt gac tgc aaa gcc tgg gct tat ttc tct gat	5686		
Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp			
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gtt gag ctg gaa aaa gat gtg cac tca ggc ctg att gga ccc ctt ctg	5734		
Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu			
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gtc tgc cac act aac aca ctg aac cct gct cat ggg aga caa gtg aca	5782		
Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr			
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gtt cag gaa ttt gct ctg ttt ttc acc atc ttt gat gag acc aaa agc	5830		
Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser			
1875	1880	1885	
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Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn			
1890	1895	1900	
atc cag atg gaa gat ccc act ttt aaa gag aat tat cgc ttc cat gca	5926		
Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala			
1905	1910	1915	1920
atc aat ggc tac ata atg gat aca cta cct ggc tta gta atg gct cag	5974		
Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln			
1925	1930	1935	
gat cca agg att cga tgg tat ctg ctc agc atg ggc agc aat gaa aac	6022		
Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn			
1940	1945	1950	
atc cat tct att cat ttc agt gga cat gtg ttc act gta cga aaa aaa	6070		
Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys			
1955	1960	1965	

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Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu	
1970 1975 1980	
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Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys	
1985 1990 1995 2000	
ctt att ggc gag cat cta cat gct ggg atg agc aca ctt ttt ctg gtg	6214
Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val	
2005 2010 2015	
tac agc aat aag tgt cag act ccc ctg gga atg gct tct gga cac att	6262
Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile	
2020 2025 2030	
aga gat ttt cag att aca gct tca gga caa tat gga cag tgg gcc cca	6310
Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro	
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aag ctg gcc aga ctt cat tat tcc gga tca atc aat gcc tgg agc acc	6358
Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr	
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aag gag ccc ttt tct tgg atc aag gtg gat ctg ttg gca cca atg att	6406
Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile	
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att cac ggc atc aag acc cag ggt gcc cgt cag aag ttc tcc agc ctc	6454
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu	
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Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp	
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cag act tat cga gga aat tcc act gga acc tta atg gtc ttc ttt ggc	6550
Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly	
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aat gtg gat tca tct ggg ata aaa cac aat att ttt aac cct cca att	6598
Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile	
2130 2135 2140	

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att gct cga tac atc cgt ttg cac cca act cat tat agc att cgc agc 6646
 Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser
 2145 2150 2155 2160

 act ctt cgc atg gag ttg atg ggc tgt gat tta aat agt tgc agc atg 6694
 Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met
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 cca ttg gga atg gag agt aaa gca ata tca gat gca cag att act gct 6742
 Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala
 2180 2185 2190

 tca tcc tac ttt acc aat atg ttt gcc acc tgg tct cct tca aaa gct 6790
 Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala
 2195 2200 2205

 cga ctt cac ctc caa ggg agg agt aat gcc tgg aga cct cag gtg aat 6836
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 aat cca aaa gag tgg ctg caa gtg gac ttc cag aag aca atg aaa gtc 6886
 Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
 2225 2230 2235 2240

 aca gga gta act act cag gga gta aaa tct ctg ctt acc agc atg tat 6934
 Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr
 2245 2250 2255

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 Val Lys Glu Phe Leu Ile Ser Ser Gln Asp Gly His Gln Trp Thr
 2260 2265 2270

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 Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
 2275 2280 2285

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 Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
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 <212> PRT
 <213> Homo sapiens

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Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
 -1 1 5 10

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
 15 20 25

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
 30 35 40 45

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
 50 55 60

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
 65 70 75

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
 80 85 90

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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
95 100 105

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
110 115 120 125

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
145 150 155

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
160 165 170

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
175 180 185

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
190 195 200 205

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
210 215 220

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
225 230 235

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
240 245 250

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
255 260 265

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
270 275 280 285

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
290 295 300

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
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335 340 345

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
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Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
370 375 380

Trp Val His Tyr Ile Ala Ala Glu Glu Asp Trp Asp Tyr Ala Pro
385 390 395

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
400 405 410

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
415 420 425

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
430 435 440 445

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
450 455 460

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
465 470 475

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
480 485 490

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
495 500 505

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
510 515 520 525

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
530 535 540

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
545 550 555

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
560 565 570

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Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
575 . 580 585

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
590 595 600 605

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
610 615 620

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
625 630 635

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
640 645 650

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
655 660 665

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
670 675 680 685

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
690 695 700

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
705 710 715

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
720 725 730

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg
735 740 745

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
750 755 760 765

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
770 775 780

Ile Gln Asn Val Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
785 790 795

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
800 805 810

-20-

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
815 820 825

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
830 835 840 845

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
850 855 860

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
865 870 875

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
880 885 890

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
895 900 905

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
910 915 920 925

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
930 935 940

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
945 950 955

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
960 965 970

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
975 980 985

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn
990 995 1000 1005

Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu
1010 1015 1020

Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr
1025 1030 1035

Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
1040 1045 1050

-21-

Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr
1055 1060 1065

Ser Ser Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile
070 1075 1080 1085

Pro Pro Asp Ala Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe
1090 1095 1100

Leu Pro Glu Ser Ala Arg Trp Ile Gln Arg Thr His Gly Lys Asn Ser
1105 1110 1115

Leu Asn Ser Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly
1120 1125 1130

Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys
1135 1140 1145

Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu
150 1155 1160 1165

Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn
1170 1175 1180

Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu
1185 1190 1195

Ile Glu Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln
1200 1205 1210

Ile His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu
1215 1220 1225

Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala
230 1235 1240 1245

Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr
1250 1255 1260

Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu
1265 1270 1275

Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys
1280 1285 1290

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Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln
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Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr
310 1315 1320 1325

Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser
1330 1335 1340

Lys Asn Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr
1345 1350 1355

Asn Glu Lys Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys
1360 1365 1370

Leu Thr Arg Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro
1375 1380 1385

Ile Ala Lys Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr
390 1395 1400 1405

Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr
1410 1415 1420

Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly
1425 1430 1435

Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
1440 1445 1450

Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser
1455 1460 1465

Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu
470 1475 1480 1485

Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr
1490 1495 1500

Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His
1505 1510 1515

Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile
1520 1525 1530

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Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val
1535 1540 1545

Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu
550 1555 1560 1565

Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu Trp Lys
1570 1575 1580

Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Asp Thr
1585 1590 1595

Ile Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile
1600 1605 1610

Asn Glu Gly Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln
1615 1620 1625

Gly Arg Thr Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg
630 1635 1640 1645

His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu
1650 1655 1660

Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe
1665 1670 1675

Asp Ile Tyr Asp Glu Asp Asn Gln Ser Pro Arg Ser Phe Gln Lys
1680 1685 1690

Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr
1695 1700 1705

Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly
710 1715 1720 1725

Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly
1730 1735 1740

Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly
1745 1750 1755

Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val
1760 1765 1770

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Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu
 1775 1780 1785
 Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn
 790 1795 1800 1805
 Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His
 1810 1815 1820
 His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 1825 1830 1835
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly
 1840 1845 1850
 Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg
 1855 1860 1865
 Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu
 870 1875 1880 1885
 Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala
 1890 1895 1900
 Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg
 1905 1910 1915
 Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val
 1920 1925 1930
 Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser
 1935 1940 1945
 Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val
 950 1955 1960 1965
 Arg Lys Iys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly
 1970 1975 1980
 Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg
 1985 1990 1995
 Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu
 2000 2005 2010

-25-

Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser
2015 2020 2025

Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln
030 2035 2040 2045

Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
2050 2055 2060

Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala
2065 2070 2075

Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe
2080 2085 2090

Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly
2095 2100 2105

Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val
110 2115 2120 2125

Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn
2130 2135 2140

Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser
2145 2150 2155

Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser
2160 2165 2170

Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln
2175 2180 2185

Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro
190 2195 2200 2205

Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro
2210 2215 2220

Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr
2225 2230 2235

Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr
2240 2245 2250

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Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His
 2255 . 2260 2265

 Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly
 270 2275 2280 2285

 Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
 2290 2295 2300

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 Leu Pro Ala Leu Leu Leu Leu Leu Phe Leu Gly Pro Trp Pro Ala
 -20 -15 -10

gcg agc cac ggc ggc aag tac tcg cgg gag aag aac cag ccc aag cgc 145
 Ala Ser His Gly Gly Lys Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro

-27-

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tcc ccg aaa cgc gag tcc gga gag gag ttc cgc atg gag aag ttg aac					
Ser Pro Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn					
15		20		25	
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sag ctg tgg gag aag gcc cag cga ctg cat ctt cct ccc gtg agg ctg					
Gln Leu Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu					
30		35		40	
					289
gcc cag ctc cac gct gat ctg aag ata cag gag agg gac gaa ctc gcc					
Ala Glu Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala					
45		50		55	
					337
tcc aag aaa cta aag ctt gac ggc ttg gac gaa gat ggg gag aag gaa					
Trp Lys Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu					
60		65		70	
					385
gct aga ctc ata cgc aac ctc aat gtc atc ttg gcc aag tat ggt ctg					
Ala Arg Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu					
75		80		85	
					90
					433
gac ggc aag aag gac gct cgg cag gtg acc agc aac tcc ctc agt ggc					
Asp Gly Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly					
95		100		105	
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acc cag gaa gac ggg ctg gat gac ccc agg ctg gaa aag ctg tgg cac					
Thr Gln Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His					
110		115		120	
					529
aag gcg aag acc tct ggg aaa ttc tcc ggc gaa gaa ctg gac aag ctc					
Lys Ala Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu					
125		130		135	
					577
tgg cgg gag ttc ctg cat cac aaa gag aaa gtt cac gag tac aac gtc					
Trp Arg Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val					
140		145		150	
					625
ctg ctg gag acc ctg agc agg acc gaa gaa atc cac gag aac gtc att					
Leu Leu Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile					
155		160		165	
					170
					673
agc ccc tcc gac ctg agc gac atc aag ggc agc gtc ctg cac agc agg					
Ser Pro Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg					
175		180		185	

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cac acg gag ctg aag gag aag ctg cgc agc atc aac cag ggc ctg gac 721
 His Thr Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp
 190 195 200

 cgc ctg cgc agg gtc agc cac cag ggc tac agc act gag gct gag ttc 769
 Arg Leu Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe
 205 210 215

 cag gag ccc agg gtg att gac ctg tgg gac ctg gcg cag tcc gcc aac 817
 Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn
 220 225 230

 ctc acg gac aag gag ctg gag gcg ttc cgg gag gag ctc aag cac ttc 865
 Leu Thr Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe
 235 240 250

 caa gcc aaa atc gag aag cac aac cac tac cag aag cag ctg gag att 913
 Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile
 255 260 265

 gcg cac gag aag ctg agg cac gca gag agc gtg ggc gac ggc gag cgt 961
 Ala His Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg
 270 275 280

 gtg agc cgc agc cgc gag aag cac gcc ctg ctg gag ggg cgg acc aag 1009
 Val Ser Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys
 285 290 295

 gag ctg ggc tac acg gtg aag aag cat ctg cag gac ctg tcc ggc agg 1057
 Glu Leu Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg
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 atc tcc aga gct cgg cac aac gaa ctc tgaaggcact gggggccca 1104
 Ile Ser Arg Ala Arg His Asn Glu Leu
 315 320

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 tggtgactgc agccgctgcc gtcgcgacac agggcttggt ggtggtagca ttgggtctg 1284
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-29-

ccaccccaagt gaggacctcg atgtccayct gctgtcaggt ctgatagtcc tctgctaaaa 1404
caacacgatt tacataaaaa atcttacaca tctgccaccq gaaataccat gcacagagtc 1464
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-15 -10 -5

Gly Lys Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg
-1 1 5 10

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu
15 20 25 30

Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His
35 40 45

Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu
50 55 60

Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile
65 70 75

Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys
80 85 90

Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp
95 100 105 110

Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr
115 120 125

Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe
130 135 140

-30-

Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr
145 150 155

Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp
160 165 170

Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu
175 180 185 190

Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg
195 200 205

Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg
210 215 220

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys
225 230 235

Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile
240 245 250

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys
255 260 265 270

Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser
275 280 285

Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr
290 295 300

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305 310 315

Arg His Asn Glu Leu
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-31-

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35 40 45Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65 70 75 80Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225 230 235 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His

-32-

245 250 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
260 265 270Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
275 280 285Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
290 295 300Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305 310 315 320Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
325 330 335Met Lys Asn Asn Gln Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
340 345 350Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
355 360 365Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
370 375 380Tyr Ile Ala Ala Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
385 390 395 400Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
405 410 415Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
420 425 430Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
435 440 445Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
450 455 460Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
465 470 475 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys

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485 490 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
500 505 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
515 520 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
530 535 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545 550 555 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
565 570 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
580 585 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
595 600 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
610 615 620

Leu Gin Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625 630 635 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
645 650 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
660 665 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
675 680 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
690 695 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
705 710 715 720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala

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725 730 735

Ile Glu Pro Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu
 740 745 750

Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp
 755 760 765

Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln
 770 775 780

Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 785 790 795 800

Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser
 805 810 815

Gly Ser Val Pro Gln Phe Lys Val Val Phe Gln Glu Phe Thr Asp
 820 825 830

Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu
 835 840 845

Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met
 850 855 860

Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser
 865 870 875 880

Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys
 885 890 895

Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln
 900 905 910

His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala
 915 920 925

Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile
 930 935 940

Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly
 945 950 955 960

Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp

-35-

965 970 975

Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg
980 985 990Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr
995 1000 1005Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu
1010 1015 1020Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
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1105 1110 1115 1120Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly
1125 1130 1135Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn
1140 1145 1150Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu
1155 1160 1165Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys
1170 1175 1180Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp
1185 1190 1195 1200

Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met

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1205 1210 1215

Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe
1220 1225 1230Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr
1235 1240 1245Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
1250 1255 1260Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala
1265 1270 1275 1280Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
1285 1290 1295Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg
1300 1305 1310Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys
1315 1320 1325Thr Met Lys Val Thr Gly Val Thr Gln Gly Val Lys Ser Leu Leu
1330 1335 1340Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
1345 1350 1355 1360His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln
1365 1370 1375Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro
1380 1385 1390Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln
1395 1400 1405Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1410 1415 1420